

GenCore version 5.1.7
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OM protein - protein search, using sw model
Run on: May 2, 2006, 18:31:17 ; Search time 231 Seconds
(without alignments)
1154.501 Million cell updates/sec
Title: US-10-696-699A-2
Perfect score: 2018
Sequence: 1 MGRVGLSPRQKALAKPE.....LLPDKASEEKKQLGNGTPK 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1827.5	90.6	403	1 S14L2 HUMAN	O76054 homo sapien
2	1824.5	90.4	403	2 Q5BEQ2 HUMAN	O53e2d homo sapien
3	1726.5	85.6	403	3 Q5EBD0 RAT	O5ebd0 rattus norv
4	1724.5	85.5	403	1 S14L2 MOUSE	O99j08 mus musculu
5	1724.5	85.5	403	2 Q5SQ25 MOUSE	O5sq25 mus musculu
6	1722.5	85.4	403	1 S14L2 RAT	O99ms0 rattus norv
7	1685.5	83.5	403	2 Q867A0 BOVIN	O867a0 bos taurus
8	1616.5	80.1	387	1 S14L2 BOVIN	P38875 bos taurus
9	1606.5	79.6	392	2 Q6PD61 HUMAN	O6pd61 homo sapien
10	1580.5	78.3	392	2 Q5REK6 PONPY	O5rek6 pongo pygma
11	1428	70.8	400	1 S14L3 HUMAN	O9udx4 homo sapien
12	1426	70.7	400	2 Q6ISB2 HUMAN	O6ish2 homo sapien
13	1425	70.6	400	2 Q6XC17 HUMAN	O6xc17 homo sapien
14	1413	70.0	400	1 S14L3 RAT	O9z1j8 rattus norv
15	1408.5	69.8	401	2 Q5SQ27 MOUSE	O5sq27 mus musculu
16	1309.5	64.9	403	1 S14L4 MOUSE	O9r0f9 mus musculu
17	1309.5	64.9	403	2 Q5SQ22 MOUSE	O5sq22 mus musculu
18	1304.5	64.6	406	1 S14L4 HUMAN	O9udx3 homo sapien
19	1259	62.4	352	2 Q6ICM2 HUMAN	O6icm2 homo sapien
20	1239	61.4	389	2 Q4RUZ5 TETNG	O4ruz5 tetraodon n
21	1169	57.9	391	2 Q4S1Y9 TETNG	O4sly9 tetraodon p
22	661.5	32.8	342	1 RALB_T0DPA	P49193 todarodes p
23	522	25.9	394	2 Q7Q6S7 ANOGA	O7q6s7 anopheles g
24	439	21.8	407	2 Q8SYC4 DROME	O8syc4 drosophila
25	433	21.5	756	2 Q43304 HUMAN	O43304 homo sapien
26	411	20.4	715	2 Q66KX9 XENTR	O66kx9 xenopus tro
27	409	20.3	715	2 Q641D9 XENLA	O641d9 xenopus lae
28	408	20.2	383	2 O17907 CAEEL	O17907 caenorhabdi
29	405	20.1	383	2 Q501B6 CAEEL	O501b6 caenorhabdi
30	399	19.8	681	2 Q6GPB3 XENLA	O6gpb3 xenopus lae
31	397	19.7	715	1 S14L1 HUMAN	O92503 homo sapien

32	395	19.6	617	2 Q4R9B6 MACFA	Q4r9b6 macaca fasc
33	394	19.5	723	2 Q59HE8 HUMAN	Q59he8 homo sapien
34	388.5	19.3	743	1 YN02 CAEEL	Q03606 caenorhabdi
35	385	19.1	630	2 Q6A071 MOUSE	Q6a071 mus musculu
36	385	19.1	716	2 Q99J07_MOUSE	Q99j07 mus musculu
37	385	19.1	719	2 Q9DBQ0_MOUSE	Q9dbq0 mus musculu
38	385	19.1	739	2 Q611N1 CAEEL	Q611n1 caenorhabdi
39	380	18.8	715	2 Q723R7 HUMAN	Q723r7 homo sapien
40	376	18.6	218	2 Q5BZ08_SCHJA	Q5bz08 schistosoma
41	375	18.6	697	2 Q803G8_BRARE	Q803g8 brachydanio
42	371	18.4	659	1 RETM DROME	Q9vnd6 drosophila
43	361.5	17.9	832	2 Q4SUFO_TETNG	Q4suf0 tetraodon n
44	352	17.4	630	2 Q5TNI6_ANOGA	Q5tni6 anopheles g
45	345	17.1	547	2 Q7PWB1_ANOGA	Q7pwb1 anopheles g

ALIGNMENTS

RESULT 1
S14L2 HUMAN
ID S14L2_HUMAN STANDARD; PRT; 403 AA.
AC O76054; Q9ULN4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE SEC14-like superinfectant protein 2 (Alpha-tocopherol associated protein) (TAP)
DE (TAP) (Superinfectant protein factor) (SPF) (Squalene transfer protein).
GN Name=SEC14L2; Synonyms=KIAA1186;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), ALTERNATIVE SPLICING, AND CHARACTERIZATION.
RX MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
RA Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J., Azzi A.;
RT "A novel human tocopherol-associated protein: cloning, in vitro expression, and characterization."
RT J. Biol. Chem. 275:25672-25680(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=21338208; PubMed=11444841; DOI=10.1006/bbrc.2001.5162;
RA Yamauchi J., Iwamoto T., Kida S., Masushige S., Yamada K., Esashi T.;
RT "Tocopherol-associated protein is a ligand-dependent transcriptional activator".
RT Biochem. Biophys. Res. Commun. 285:295-299(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX PubMed=11226224; DOI=10.1073/pnas.041620398;
RA Shibata N., Arita M., Misaki Y., Dohmae N., Takio K., Ono T., Inoue K., Arai H.;
RT "Supernatant protein factor, which stimulates the conversion of squalene to lanosterol, is a cytosolic squalene transfer protein and enhances cholesterol biosynthesis".
RT Proc. Natl. Acad. Sci. U.S.A. 98:2244-2249(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX PubMed=15461802; DOI=10.1186/gb-2004-5-10-r84;
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A., Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J., Beare D.M., Dunham I.;
RT "A genome annotation-driven approach to cloning the human ORFeome.";
RT Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).

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RN  [6] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX  MEDLINE=2057165; PubMed=10591208; DOI=10.1038/990031;
RA  Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA  Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA  Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA  Bird C.P., Blakey S.B., Bridgeman A.M., Buck D., Bursley J.,
RA  Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA  Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA  Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA  Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA  Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA  Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA  Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA  Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,
RA  Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA  Martyn I.D., Mashreghi-Mohammadi M., Matheva L.H., McCann O.T.,
RA  Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA  Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA  Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA  Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA  Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,
RA  Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA  Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA  Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA  Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA  Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA  Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA  Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA  Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA  Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA  Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA  Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA  Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA  Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA  Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA  Schorf F., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA  Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA  Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA  Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA  Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanaki J.P.,
RA  Peyrard M., Kedra D., Serousi E., Fransson I., Tapia I., Bruder C.E.,
RA  O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA  Khan A.S., Lane L., Tilahun Y., Wright H.;
RT  "The DNA sequence of human chromosome 22."
RL  Nature 402:489-495(1999).
[7]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 191-360 (ISOFORM 2).
RC  TISSUE=Brain;
RX  MEDLINE=20039618; PubMed=10574461;
RA  Hiroseawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA  Ohara O.;
RT  "Characterization of cDNA clones selected by the GeneMark analysis
RT  from size-fractionated cDNA libraries from human brain.";
RL  DNA Res. 6:329-336(1999).
CC  -!- FUNCTION: Carrier protein. Binds to some hydrophobic molecules and
CC  promotes their transfer between the different cellular sites.
CC  Binds with high affinity to alpha-tocopherol. Also binds with a
CC  weaker affinity to other tocopherols and to tocotrienols. May have
CC  a transcriptional activatory activity via its association with
CC  alpha-tocopherol. Probably recognizes and binds some squalene
CC  structure, suggesting that it may regulate cholesterol
CC  biosynthesis by increasing the transfer of squalene to a metabolic
CC  active pool in the cell.
CC  -!- SUBUNIT: Monomer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol,
CC  and nuclear in presence of alpha-tocopherol.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=3;
CC  Name=1;
CC  IsoId=O76054-1; Sequence=Displayed;
CC  Name=2;
CC  IsoId=O76054-2; Sequence=VSP_006031;
CC  Name=3;
CC  IsoId=O76054-3; Sequence=Not described;
CC  -!- TISSUE SPECIFICITY: Widely expressed. Strong expression in liver,
CC  brain and prostate.
CC  -!- DEVELOPMENTAL STAGE: Low expression in fetal tissues.
CC  -!- SIMILARITY: Contains 1 CRAL-TRIO domain.
CC  -!- SIMILARITY: Contains 1 GOLD domain.
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  EMBL; AL096881; CAB51405.1; -; mRNA.
CC  EMBL; CR456571; CAG30457.1; -; mRNA.
CC  EMBL; AC004832; AAF19256.1; -; Genomic DNA.
CC  EMBL; AB033012; BAA86500.1; -; mRNA.
CC  PIR; JC7708; JC7708
CC  PDB; 1O6U; X-ray; A/C/B=1-403.
CC  PDB; 1OLM; X-ray; A/C/B=1-403.
CC  Ensembl; ENSG00000100003; Homo sapiens.
CC  HGNC; HGNC:10699; SEC14L2.
CC  MIM; 607558; -; Cytosolasm; NAS.
CC  GO; GO:0005737; C:cytoplasm; NAS.
CC  GO; GO:0005634; C:nucleus; NAS.
CC  GO; GO:0005386; F:carrier activity; NAS.
CC  GO; GO:0005543; F:phospholipid binding; NAS.
CC  GO; GO:0016563; F:transcriptional activator activity; NAS.
CC  GO; GO:0008431; F:vitamin E binding; NAS.
CC  GO; GO:0045893; P:positive regulation of cholesterol biosynthesis; NAS.
CC  GO; GO:0045540; P:regulation of cholesterol biosynthesis; NAS.
CC  InterPro; IPR001071; CRAL_bd_toc_tran.
CC  InterPro; IPR008273; CRAL_bd_TRIO_N.
CC  InterPro; IPR000348; Emp24_gp25L_D24.
CC  InterPro; IPR009038; GOLD.
CC  Pfam; PF00650; CRAL_TRIO; 1.
CC  Pfam; PF03765; CRAL_TRIO_N; 1.
CC  Pfam; PF01105; EMP24_GP25L; 1.
CC  PRINTS; PR00180; CRETINALDHP.
CC  SMART; SM00516; SEC14; 1.
CC  PROSITE; PS50191; CRAL_TRIO; 1.
CC  PROSITE; PS50866; GOLD; 1.
CC  3D-structure; Activator; Alternative splicing; Lipid-binding;
CC  Nuclear protein; Transcription; Transcription regulation; Transport.
CC  FT DOMAIN 76 249 CRAL-TRIO.
CC  FT DOMAIN 275 383 Missing (in isoform 2).
CC  FT VARSPLIC 361 403 /FTId=VSP_006031.
CC  FT CONFLICT 36 36 Y -> H (in Ref. 2).
CC  SQ SEQUENCE 403 AA; 46145 MW; D846747EC9D1513E CRC64;
Query Match 90.6%; Score 1827.5; DB 1; Length 403;
Best Local Similarity 87.1%; Pred No. 2.7e-140;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;
QY 1 MSGRGVGLSPRQKEALAK-----PEASTCRSRPPCSGMSSES----- 39
Db 1 MSGRGVGLSPRQKEALAKFRENVDVLPALPNPDDYFLLRWLRARSFDLQKSEAMLRKHV 60
QY 40 ----KRTLTTSLAWQPPPEVIQOYLSGGMGVDLDCPWWYDIIGPKDAKGLLPSASKQDL 95
Db 61 EFRKQIDNTIISWQPPPEVIQOYLSGGMGVDLDCPWWYDIIGPKDAKGLLPSASKQDL 120
QY 96 LFTKMRCELLQECACHOTTKLGRKVEITITTYDCEGLGKHLKWPVAVAYGEFLCMFEE 155
Db 121 LFTKMRCELLQECACHOTTKLGRKVEITITTYDCEGLGKHLKWPVAVAYGEFLCMFEE 180
QY 156 NYPETLKLFFVVKAPKLPFPVYVNLKPFSEDRKIKIYVLGANYKEVLLKHTSPQVPVE 215
Db 181 NYPETLKLFFVVKAPKLPFPVYVNLKPFSEDRKIKIYVLGANYKEVLLKHTSPQVPVE 240
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QY 216 YGGTMTDPGPNPKCKSKINYGDI PRKYVVRDQVQKQYEHVSQISRGSSHQVEYELLFPG 275
 Db 241 YGGTMTDPGPNPKCKSKINYGDI PRKYVVRDQVQKQYEHVSQISRGSSHQVEYELLFPG 300
 QY 276 CVLRWQFMSDGDVGFGLFKTKMGERQAGEMTEVLPNQRNYSNHLVPEDGTLTCSDPGI 335
 Db 301 CVLRWQFMSDGDVGFGLFKTKMGERQAGEMTEVLPNQRNYSNHLVPEDGTLTCSDPGI 360
 QY 336 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEKKKQLGAGTPK 378
 Db 361 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEKKKQLGAGTPK 403
 RESULT 2
 Q53EQ2 HUMAN PRELIMINARY; PRT; 403 AA.
 ID Q53EQ2
 AC Q53EQ2
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE SEC14-like 2 variant (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP [1]
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaracne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 FT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 SQ SEQUENCE 403 AA; 46117 MW; 962F64C43F7DD218 CRC64;

Query Match 90.4%; Score 1824.5; DB 2; Length 403;
 Best Local Similarity 86.8%; Pred. No. 4.8e-140;
 Matches 350; Conservative 10; Mismatches 18; Indels 25; Gaps 2;
 QY 1 MSRGVGDLSPROKEALAK-----PEASTCRSRRPCSGMSSSES----- 39
 Db 1 MSRGVGDLSPROKEALAKFRENVDVLPALPNPDYFLLWLRARSFDLQKSEAMLRKHV 60
 QY 40 ----KRTLTSLAWQPPEVIOQYLSGGMCGYDLDCFPWYDIIGPKDAKGLLFSASKODL 95
 Db 61 EFRKQKIDNIISWQPEVIOQYLSGGMCGYDLDCFPWYDIIGPKDAKGLLFSASKODL 120
 QY 96 LRTKWRCELLQSCAHTTKLGRKVTITIIYDCGLGLKHLWKPAVEAYGEFLCMFEE 155
 Db 121 LRTKWRCELLQSCAHTTKLGRKVTITIIYDCGLGLKHLWKPAVEAYGEFLCMFEE 180
 QY 156 NYPETLKRFLFVKAPKLPVAVNYLIKPLSDTRKKIWLGNKVEVLLKHISPDQVPVE 215
 Db 181 NYPETLKRFLFVKAPKLPVAVNYLIKPLSDTRKKIWLGNKVEVLLKHISPDQVPVE 240
 QY 216 YGGTMTDPGPNPKCKSKINYGDI PRKYVVRDQVQKQYEHVSQISRGSSHQVEYELLFPG 275
 Db 241 YGGTMTDPGPNPKCKSKINYGDI PRKYVVRDQVQKQYEHVSQISRGSSHQVEYELLFPG 300

QY 276 CVLRWQFMSDGDVGFGLFKTKMGERQAGEMTEVLPNQRNYSNHLVPEDGTLTCSDPGI 335
 Db 301 CVLRWQFMSDGDVGFGLFKTKMGERQAGEMTEVLPNQRNYSNHLVPEDGTLTCSDPGI 360
 QY 336 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEKKKQLGAGTPK 378
 Db 361 YVLRFDNTYSFTHAKKNFTVEVLLPDKASEKKKQLGAGTPK 403
 RESULT 3
 Q5EBD0 RAT PRELIMINARY; PRT; 403 AA.
 ID Q5EBD0
 AC Q5EBD0
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE SEC14-like 2.
 GN Name=Sec14l2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP [1]
 RA Tissue=Liver;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaracne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 SQ SEQUENCE 403 AA; 46205 MW; D83CCF10DBA4837 CRC64;

Query Match 85.6%; Score 1726.5; DB 2; Length 403;
 Best Local Similarity 81.1%; Pred. No. 4.7e-132;
 Matches 327; Conservative 25; Mismatches 26; Indels 25; Gaps 2;
 QY 1 MSRGVGDLSPROKEALAK-----PEASTCRSRRPCSGMSSSES----- 39
 Db 1 MSRGVGDLSPROKEALAK-----PEASTCRSRRPCSGMSSSES----- 39


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Query Match      85.4%; Score 1722.5; DB 1; Length 403;
Best Local Similarity 81.1%; Pred. No. 9.9e-132;
Matches 327; Conservative 25; Mismatches 26; Indels 25; Gaps 2;

QY 1 MSGRVGDLSPKQKEALAK-----PEASTCRSRPCSGSMWSES----- 39
DB 1 MSGRVGDLSPKQKEALAKFRENVDVLPALPNPDDYFLRLWLRLARSFDLQKSEAMLRKHV 60

QY 40 ----KRTLTTSIAWOPPEVIOYLSGGMCGYDLDCGPVWYDIIGPKDAKGLLFSASKQDL 95
DB 61 EFRKQKIDKIISWQPEVIOYLSGGRCGYDLDCGPVWYDIIGPLDAKGLLFSASKQDL 120

QY 96 LRTKRECELLLOECACHQTTKLGRKVETITIIYDCGELGLKHLWPAVEAYGEFLCMFEE 155
DB 121 LRTKRDCELLLOECQTQAKLGKKTETITMIYDCGELGLKHLWPAVEAYGEFTLMFEE 180

QY 156 NYPETLKRFLFVVKAPKLPFVAYNLKPFLESDTRKKIMVLGANYKEVLLKHISPPQVPVE 215
DB 181 NYPETLKRFLFVVKAPKLPFVAYNLKPFLESDTRKKIMVLGANYKEVLLKHISPPQVPVE 240

QY 216 YGGTMTDPDGNPKCKSKINYGDDIPRKYVVRDQVQYEHVSQVSRGSSHQVEYELPPG 275
DB 241 YGGTMTDPDGNPKCKSKINYGDDIPKQYVVRDQVQYEHVSQVSRGSSHQVEYELPPG 300

QY 276 CVLRWQFMSGDADVGFIFLTKMGERQKAGEMTEVLPNQRVNSHLVPEDGTLTCSDPGI 335
DB 301 CVLRWQFMSGDADVGFIFLTKMGERQKAGEMTEVLPNQRVNSHLVPEDGTLTCSDPGI 360

QY 336 YVLRFDNTYSFIHAKKVNFTVEVLLPKDASEEKMQLGAGTPK 378
DB 361 YVLRFDNTYSFIHAKKVNFTVEVLLPKDASEEKLMOQOGAVTPK 403

RESULT 7
Q867A0_BOVIN
ID Q867A0_BOVIN PRELIMINARY; PRT; 403 AA.
AC Q867A0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Liver tocopherol-associated protein.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
RA Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.,
RA Azzi A.;
RT "A novel human tocopherol-associated protein: cloning, in vitro
RT expression, and characterization.";
RL J. Biol. Chem. 275:25672-25680(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Breyer I., Schittny J.C., Schuerch S., Zimmermann A., Stocker A.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF432353; AAC031942.1; -; mRNA.
DR HSSP; 076054; 106U.
DR SMR; Q867A0; 1-397.
DR GO; GO:0003622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008289; F:lipid binding; IEA.
DR GO; GO:0008320; F:protein carrier activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0008886; P:intracellular protein transport; IEA.
DR GO; GO:0008810; P:transport; IEA.
DR InterPro; IPR001251; CRAL_TRIO_C.
DR InterPro; IPR008273; CRAL_TRIO_N.
DR InterPro; IPR000348; Emp24_gp25L_p24.
DR InterPro; IPR009038; GOLD.
DR InterPro; IPR001071; RetBind/tocTrans.
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DR Pfam; PF00650; CRAL_TRIO; 1.
DR Pfam; PF03765; CRAL_TRIO_N; 1.
DR Pfam; PF01105; EMP24_GP25L; 1.
DR PRINTS; PRO0180; CRETINALDHP.
DR SMART; SM00516; SEC14; 1.
DR PROSITE; PS50191; CRAL_TRIO; 1.
DR PROSITE; PS50866; GOLD; 1.
SQ SEQUENCE 403 AA; 46200 MW; 67C28BFC173E1CD9 CRC64;

Query Match      83.5%; Score 1685.5; DB 2; Length 403;
Best Local Similarity 78.2%; Pred. No. 1e-128;
Matches 315; Conservative 34; Mismatches 29; Indels 25; Gaps 2;

QY 1 MSGRVGDLSPKQKEALAK-----PEASTCRSRPCSGSMWSES----- 39
DB 1 MSGRVGDLSPKQKEALAKFRENVDVLPALPNPDDYFLRLWLRLARNFNLQKSEAMLRKHV 60

QY 40 ----KRTLTTSIAWOPPEVIOYLSGGMCGYDLDCGPVWYDIIGPKDAKGLLFSASKQDL 95
DB 61 EFRKQKIDNIMSWQPEVIOYLSGGMCGYDLDCGPVWYDIIGPLDAKGLLFSASKQDL 120

QY 96 LRTKRECELLLOECACHQTTKLGRKVETITIIYDCGELGLKHLWPAVEAYGEFLCMFEE 155
DB 121 LRTKRDCELLLOECVROTETKMGKKEATTLIYDCGELGLKHLWPAVEAYGEFLCMFEE 180

QY 156 NYPETLKRFLFVVKAPKLPFVAYNLKPFLESDTRKKIMVLGANYKEVLLKHISPPQVPVE 215
DB 181 NYPETLKRFLFVVKAPKLPFVAYNLKPFLESDTRKKIQVLGANWKEVLLKYISPDQLPVE 240

QY 216 YGGTMTDPDGNPKCKSKINYGDDIPRKYVVRDQVQYEHVSQVSRGSSHQVEYELPPG 275
DB 241 YGGTMTDPDGNPKCKSKINYGDDIPKQYVVRDQVQYEHVSQVSRGSSHQVEYELPPG 300

QY 276 CVLRWQFMSGDADVGFIFLTKMGERQKAGEMTEVLPNQRVNSHLVPEDGTLTCSDPGI 335
DB 301 CVLRWQFMSGDADVGFIFLTKMGERQKAGEMREVLPQRYNAHLVPEDGSLTCSDPGI 360

QY 336 YVLRFDNTYSFIHAKKVNFTVEVLLPKDASEEKMQLGAGTPK 378
DB 361 YVLRFDNTYSFIHAKKVNFTVEVLLPKDASEEKMQLGAVTPK 403

RESULT 8
S14L2_BOVIN
ID S14L2_BOVIN STANDARD; PRT; 387 AA.
AC P58875;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP)
DE (bTAP) (Fragment).
GN Name=SEC14L2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Meadus J., MacInnis R., Dubeski P., Hidioglu N., Madere R.;
RT "Induction of hepatic tocopherol associated protein (TAP) mRNA but not
RT alpha-tocopherol transfer protein (TTP) mRNA in cattle fed increasing
RT levels of vitamin E.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PROTEIN SEQUENCE OF 178-195 AND 335-353.
RX MEDLINE=20400504; PubMed=10829015; DOI=10.1074/jbc.M000851200;
RA Zimmer S., Stocker A., Sarbolouki M.N., Spycher S.E., Sassoon J.,
RA Azzi A.;
RT "A novel human tocopherol-associated protein: cloning, in vitro
RT expression, and characterization.";
RL J. Biol. Chem. 275:25672-25680(2000).
```


CC -1- FUNCTION: Carrier protein. Binds to some hydrophobic molecules and
 CC promotes their transfer between the different cellular sites.
 CC Binds with high affinity to alpha-tocopherol. Also binds with a
 CC weaker affinity to other tocopherols and to tocotrienols. May have
 CC a transcriptional activatory activity via its association with
 CC alpha-tocopherol. Probably recognizes and binds some squalene
 CC structure, suggesting that it may regulate cholesterol
 CC biosynthesis by increasing the transfer of squalene to a metabolic
 CC active pool in the cell (By similarity).
 CC
 CC -1- SUBUNIT: Monomer.
 CC
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic in absence of alpha-tocopherol,
 CC and nuclear in presence of alpha-tocopherol (By similarity).
 CC
 CC -1- SIMILARITY: Contains 1 CRAL-TRIO domain.
 CC
 CC -1- SIMILARITY: Contains 1 GOLD domain.
 CC
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC -----
 CC EMBL; AF487977; AAL90886.1; -; mRNA.
 CC SNMR; P58875; 1-387.
 CC DR GO; GO:0005737; C:cytoplasm; ISS.
 CC DR GO; GO:0005634; C:nucleus; ISS.
 CC DR GO; GO:0005543; F:phospholipid binding; ISS.
 CC DR GO; GO:0008320; F:protein carrier activity; ISS.
 CC DR GO; GO:0016563; F:transcriptional activator activity; ISS.
 CC DR GO; GO:0008431; F:vitamin E binding; ISS.
 CC DR GO; GO:0045893; P:positive regulation of transcription, DNA-d. .; ISS.
 CC DR GO; GO:0045540; P:regulation of cholesterol biosynthesis; ISS.
 CC DR InterPro; IPR001071; CRAL_bd_toc_tran.
 CC DR InterPro; IPR001251; CRAL_bd_TRIO_C.
 CC DR InterPro; IPR000348; Emp24_gp25L_p24.
 CC DR InterPro; IPR009038; GOLD.
 CC DR Pfam; PF00650; CRAL_TRIO; 1.
 CC DR Pfam; PF03745; CRAL_TRIO_N; 1.
 CC DR Pfam; PF01105; EMP24_GP25L; 1.
 CC DR PRINTS; PR00180; CRETINALDHP.
 CC DR SMART; SM00516; SEC14; 1.
 CC DR PROSITE; PS50191; CRAL_TRIO; 1.
 CC DR PROSITE; PS50866; GOLD; 1.
 CC Activator; Direct protein sequencing; Lipid-binding; Nuclear protein;
 CC Transcription; Transcription regulation; Transport.
 CC CRAL-TRIO.
 CC FT DOMAIN 76 249
 CC FT DOMAIN 275 383 GOLD.
 CC FT CONFLICT 193 193 K -> G (in Ref. 2).
 CC FT CONFLICT 343 343 S -> N (in Ref. 2).
 CC FT NON_TER 387 387
 CC SQ SEQUENCE 387 AA; 44406 MW; FAE72E8A83CB9E9C CRC64;
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 CC Query Match 80.1%; Score 1616.5; DB 1; Length 387;
 CC Best Local Similarity 77.5%; Pred. No. 4.1e-123;
 CC Matches 300; Conservative 35; Mismatches 27; Indels 25; Gaps 2;
 CC
 CC QY 1 MSGRVGDLSPKQKALAK-----PEASTCSRPRPCSGSMWSSS----- 39
 CC DB 1 MSGRVGDLSPKQKALAKFRENVDLPALPNPDYFLRLWRARNFNLOKSEAMLRKHV 60
 CC
 CC QY 40 ----KRTLTTSLANQPVEIQYLSGGMGVYDLCPCWYDIIGPKDAKGLLPFSASKODL 95
 CC DB 61 EFRKQKIDNIMSWOPPEVQYLSGGMGVYDLCPCWYDIIGPKDAKGLLPFSASKODL 120
 CC
 CC QY 96 LRTKMRCELLQSCAHTTKLGRKVTITIIYDCGLGLKHLWKPAVEAYGEFLCMFEE 155
 CC DB 121 PKTKMRCELLQSCVQTKRQKKEATIIYDCGLGLKHLWKPAVEAYGEFLCMFEE 180
 CC
 CC QY 156 NYPETLKRFLFVVKAPKLPFVAYNLKIPFLSDTKKKIIVLGANYKEVLLKHSIDPQVPE 215
 CC DB 181 NYPETLKRFLFVVKAPKLPFVAYNLKIPFLSDTKKKIIVLGANYKEVLLKHSIDPQVPE 240
 CC
 CC QY 216 YGTTMTDPDGNPKCKSKINYGGDIPKYYVDRQVQYEHVSQISRGSSHQVEYELLFPG 275

DB 241 YGTTMTDPDGNPKCKSKINYGGDIPKYYVDRQVQYEHVSQISRGSSHQVEYELLFPG 300
 QY 276 CVLRQGFMSDGVGFGIFLTKMGERORAGMTVELPNQRVNSHLVPDGTLTCSDDPGI 335
 DB 301 CVLRQGFMSDGVGFGIFLTKMGERORAGMTVELPNQRVNSHLVPDGTLTCSDDPGI 360
 QY 336 YVLRFDNTYSFTHAKKVNFTVEVLLPD 362
 DB 361 YVLRFDNTYSFTHAKKVNFTVEVLLPD 387
 RESULT 9
 Q6PD61 HUMAN
 ID Q6PD61 HUMAN PRELIMINARY; PRT; 392 AA.
 AC Q6PD61_27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE SEC14L2 protein.
 GN Name=SEC14L2;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 RN NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RC Director MGC Project;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC058915; AAH58915.1; -; mRNA.
 DR SNR; Q6PD61.1-360
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008289; F:lipid binding; IEA.
 DR GO; GO:0008320; F:protein carrier activity; IEA.
 DR GO; GO:0019841; F:retinol binding; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006886; P:intracellular protein transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR GO; GO:0007601; P:visual perception; IEA.
 DR InterPro; IPR001251; CRAL_TRIO_C.
 DR InterPro; IPR008273; CRAL_TRIO_N.
 DR InterPro; IPR000348; Emp24_gp25L_p24.
 DR InterPro; IPR001071; RetBind/tocTrans.
 DR Pfam; PF00650; CRAL_TRIO; 1.
 DR Pfam; PF03745; CRAL_TRIO_N; 1.
 DR Pfam; PF01105; EMP24_GP25L; 1.

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DR PRINTS: PR00180; CRETINALDHP.  
DR SMART; SMO0516; SEC14; 1.  
DR PROSITE; PS0191; CRAL_TRIO; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 392 AA; 44768 MW; 11A833345968FESA CRC64;  
  
Query Match 79.6%; Score 1606.5; DB 2; Length 392;  
Best Local Similarity 85.6%; Pred. No. 2.7e-122; Mismatches 9; Indels 25; Gaps 2;  
Matches 308; Conservative 9; Mismatches 18; Indels 25; Gaps 2;  
  
QY 1 MSRGVGLSPQKEALAK-----PEASTCRSRPPCGSGMWSSSES----- 39  
DB 1 MSRGVGLSPQKEALAKFRENVDVLPALPNDDYFLLRWLRARSFDLQKSEAMLRKHV 60  
  
QY 40 ----KRTLTTSIAWQPEVIQOYLGGMCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL 95  
DB 61 EFRKQKIDNIISQWPEVIQOYLGGMCGYLDGCPVWYDIIGPLDAKGLLFSASKQDL 120  
  
QY 96 LRTKMRECELLQECACHQTTKLGRKVETITIIYDCEGLGLKHLKWPAVEAYGEFLCMPEE 155  
DB 121 LRTKMRECELLQECACHQTTKLGRKVETITIIYDCEGLGLKHLKWPAVEAYGEFLCMPEE 180  
  
QY 156 NYPETLKRFLVVKAPKLPFVAYNLIKPFLSEDTTRKKIMVLGANYKEVLLKHISPDQVPVE 215  
DB 181 NYPETLKRFLVVKAPKLPFVAYNLIKPFLSEDTTRKKIMVLGANYKEVLLKHISPDQVPVE 240  
  
QY 216 YGGTWTDPGPNCKSKINYGDIIPRKYVVRDQVQYEHSHVQISRGSSHQVEYELPPG 275  
DB 241 YGGTWTDPGPNCKSKINYGDIIPRKYVVRDQVQYEHSHVQISRGSSHQVEYELPPG 300  
  
QY 276 CVLRWQFMSGDADVGFGLTKMGERORAGTEVLNQRVNSHLVPEDGTLTCDPGI 335  
DB 301 CVLRWQFMSGDADVGFGLTKMGERORAGTEVLNQRVNSHLVPEDGTLTCDPGI 360  
  
RESULT 10  
Q5REK6 PONPY PRELIMINARY; PRT; 392 AA.  
AC Q5REK6;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DE Hypothetical protein DKFZp459B2422.  
GN NamesDKFZp459B2422;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pongo.  
OX NCBI_TaxID=9600;  
RN [1]_TaxID=9600;  
RP NUCLEOTIDE SEQUENCE.  
RC The German cDNA Consortium;  
RG Ottenwaelder B., Obermaier B., Deutschenbaur S., Schaiipp A.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR857519; CAH89801.1; -, mRNA.  
DR SMR; Q5REK6; 1-360.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0008289; F:lipid binding; IEA.  
DR GO; GO:0008320; F:protein carrier activity; IEA.  
DR GO; GO:0019841; F:retinol binding; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006886; P:intracellular protein transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR GO; GO:0007601; P:visual perception; IEA.  
DR InterPro; IPR001251; CRAL_TRIO.C.  
DR InterPro; IPR008273; CRAL_TRIO.N.  
DR InterPro; IPR000348; Emp24_gp25L_p24.  
DR InterPro; IPR001071; RetBind/tocTrans.  
DR Pfam; PF00650; CRAL_TRIO; 1.  
DR Pfam; PF03765; CRAL_TRIO.N; 1.  
DR Pfam; PF01105; EMP24_gp25L; 1.
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RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey K., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L., Swann R.M.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuoyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilihan Y., Wright H.,
RT Nature 402:489-495(1999).
CC -!- FUNCTION: Probable hydrophobic ligand-binding protein; may play a
CC role in the transport of hydrophobic ligands like tocopherol,
CC squalene and phospholipids.
CC -!- SIMILARITY: Contains 1 CRAL-TRIO domain.
CC -!- SIMILARITY: Contains 1 GOLD domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: AY158086; AAC01870.1; -; mRNA.
CC ENBL: AAC004832; AAF19258.1; -; Genomic_DNA.
CC SNR; Q9UDX4; 1-397.
CC Ensembl: ENSG00000100012; Homo sapiens.
CC HGNC: HGNC:18655; SEC14L3.
CC InterPro: IPR001071; CRAL bd toc tran.
CD InterPro: IPR001251; CRAL bd TRIO C.
CD InterPro: IPR008273; CRAL bd TRIO N.
CD InterPro: IPR000348; Emp24_gp25L_p24.
CD InterPro: IPR009038; GOLD.
CD Pfam: PF00650; CRAL TRIO; 1.
CD Pfam: PF03765; CRAL TRIO N; 1.
CD Pfam: PF01105; EMP24 GP25L; 1.
CD PRINTS; PR00180; CRETINALDHP.
CD PROSITE; PSS0191; CRAL TRIO; 1.
CD PROSITE; PSS0866; GOLD; 1.
KW Lipid-binding; Polymorphism; Transport.
FT DOMAIN 76 249
FT VARIANT 275 383
FT VARIANT 335 335
FT D-> E (in dbSNP:2240345).
FT /FTID=VAR_022097.
SQ SEQUENCE 400 AA; 46048 MW; 07F880D25B66CC19 CRC64;
Query Match 70.8%; Score 1428; DB 1; Length 400;
Best Local Similarity 66.4%; Pred No. 9.8e-108;
Matches 267; Conservative 51; Mismatches 56; Indels 28; Gaps 4;
QY 1 MSGRVGDLSPQKEALAK-----PEASTCSRPRPCSGMWSSES----- 39
Db 1 MSGRVGDLSPQKEALAKFRENVDVLPALPNPDYFLLRWLARNFDLQSEALLRKYM 60
QY 40 --KRTLTS--LAWQPEVYQVYLSGMCVGYLDGCPVWYDIIGPKDAKGLFSASKQDL 95

Db 61 EPRKMTDIDHILDMQPEVIQKMPGGLGCGYDRDCGVPVWYDIIGPLDKGLFSVTQDL 120
QY 96 LETKRECELLLOECAHOHTTKLGRKVEITIIYDCGGLGKHLKWPAAVEAYGEFLCMPRE 155
Db 121 LKTRNRDCERILHECDLQTERLGKKIETIYVIFDCGGLGKHLKWPALVEVYQEFGLLEE 180
QY 156 NYPETLKEFLVVKAPKLPFVATNLIKPFSEDRKIKMVLGANYKEVLLKHSPOQVPE 215
Db 181 NYPETLKFMILIVKATKLPVGNLMKPFSEDRKIKIIVGNWKEGLKLIISPELPAQ 240
QY 216 YGGTWTDDGPNCKSKINYGDIIPKYYVRQVQOYHSHVQISRGSSHQVEYELFPQ 275
Db 241 FGGTLTDPDGNPKCLTKINYGGEIPKSMYVRQVQTOYHSHVQINRGSSHQVEYELFPQ 300
QY 276 CVLRWQFMSDGDVGGIFLTKMGORAGTMTVLNORYNHSLVPDGTLTTCSDPGI 335
Db 301 CVLRWQFSSDGDADIGFGLTKMGORAGTMTVLNORYNHSLVPDGTLTTCSEAGV 360
QY 336 YVLRFDNTYSFTHAKKVNFTVEVLLPKASEEKMKQLGAGTP 377
Db 361 YVLRFDNTYSFVHAKKVSFTVEVLLPDGCMQKYDEL---TP 399
RESULT 12
Q6ISB2 HUMAN
ID Q6ISB2_HUMAN PRELIMINARY; PRT; 400 AA.
AC Q6ISB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SEC14-like 3.
GN Name=SEC14L3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones;
RC MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC069641; AAH69641.1; -; mRNA.
DR HSP; P24280; IAUA.
DR SNR; Q6ISB2; 1-397.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008320; F:protein carrier activity; IEA.

RX MEDLINE=99277573; PubMed=10350070; DOI=10.1016/S0014-5793(99)00470-6;
RA Markulova M.I., Andreeva S.G., Shuvaeva T.M., Novoselov S.V.,
RA Peshenko I.V., Bystrova M.F., Novoselov V.I., Pesenko E.E.,
RA Lipkin V.M.;
RT "A novel 45 kDa secretory protein from rat olfactory epithelium:
RL primary structure and localization.";
RL FEBS Lett. 450:126-130(1999).
CC -1- FUNCTION: Probable hydrophobic ligand-binding protein; may play a
CC role in the transport of hydrophobic ligands like tocopherol,
CC squalene and phospholipids.
CC -1- TISSUE SPECIFICITY: Detected in a layer of supportive cells in
CC olfactory epithelium, in the apical region of the trachea and in
CC the surface layer of ciliated bronchial epithelium in the lung.
CC -1- PTM: The N-terminus seems to be blocked.
CC -1- SIMILARITY: Contains 1 CRAL-TRIO domain.
CC -1- SIMILARITY: Contains 1 GOLD domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AJ132352; CAA10644.1; -; mRNA.
DR HSSP: P24280; 1AUA.
DR SMR: Q9Z1J8; 1-392.
DR InterPro: IPR001071; CRAL_bd_toc_tran.
DR InterPro: IPR001251; CRAL_bd_TRIO_C.
DR InterPro: IPR008273; CRAL_bd_TRIO_N.
DR InterPro: IPR000348; Emp24_gp25L_p24.
DR InterPro: IPR009038; GOLD.
DR Pfam: PF00650; CRAL_TRIO; 1.
DR Pfam: PF03765; CRAL_TRIO_N; 1.
DR Pfam: PF01105; EMP24_GP25L; 1.
DR PRINTS: PR00180; CRETINALDHP.
DR SMART: SM00516; SEC14; 1.
DR PROSITE: PS00191; CRAL_TRIO; 1.
DR PROSITE: PS00866; GOLD; 1.
DR Direct protein sequencing; Lipid-binding; Transport.
KW DOMAIN 76 249 CRAL-TRIO.
FT DOMAIN 275 383 GOLD.
SQ SEQUENCE 400 AA; 548A72DDA9B4FC36 CRC64;

Query Match 70.0%; Score 1413; DB 1; Length 400;
Best Local Similarity 65.9%; Pred. No. 1.6e-106;
Matches 265; Conservative 52; Mismatches 57; Indels 28; Gaps 4;

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DB 1 MSGRVGDLSPROKEALAKFRENVDVLPALPNPDYFLLRLARNFQKSEAMLRKYM 60

QY 40 --KRTLTTS--LAWQPEVIQOYLGGMCGYDLDCPWWYDIIGPKDAKGLLFSASKODL 95
DB 61 EFRKTMIDHLDHQPEVIQYKMPGGLCGYDRDGCPCWYDIIGPLPKGLLFSVTKODL 120

QY 96 LRTKMRCELLQECAGHTTKLGRKVTITIIYDCGGLGLKHLWKPAVEAYGEFLCMFEE 155
DB 121 LKTRMDCERILHECDLQTERLGRKTIETIIVIFDCGGLGLKHLWKPAVEAYGEFLLEE 180

QY 156 NYPETLKLFLVWAKPLFPVAYNLIKPFLSDTRKKIMVLGAN-YKEVLLKHISPDQVPE 215
DB 181 NYPETLKPMLIVKATKLPFGVGNLMPFLSDTRRKIVVLGNSWKEGLLKLIPEELPAH 240

QY 216 YGGTMTDPDGNPKCKSKINYGDIIPRKYIVRDQVKQYEHVSQISRGSSHQVEYELLFPG 275
DB 241 FGGTLTDPDGNPKCLTKINYGGEIPKSMYVRDQVKQYEHVSQISRGSSHQVEYELLFPG 300

QY 276 CVLRWQFSSGDADVGFGIFLTKMGERQKAGEMTEVLVLPNQRVNSHLVPEDGTLTCSDPGI 335
DB 301 CVLRWQFSSGDADIGFVFLTKMGERQKAGEMTEVLTSQRYNAHVPEDGSLTCTEAGV 360

QY 336 YVLRPDNTYSFIHAKKNFTVEVLLPDKASEKMKQLGAGTP 377

Db 361 YVLRPDNTYSFVHAKKVSTFTVEVLLPDDEGMQKYDBEL----TP 399

RESULT 15
QSSQ27_MOUSE PRELIMINARY; PRT; 401 AA.
AC QSSQ27;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein, ortholog of human and rat SEC14-like 3 (S. cerevisiae)
DE SEC14L3.
GN Name=OTTMUSP0000005238; ORFNames=RP23-81P12.8-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Matthews L;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL807395; CAI26047.1; -; Genomic_DNA.
DR SMR; QSSQ27; 1-398.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008320; F:protein carrier activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006886; P:intracellular protein transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro: IPR001251; CRAL_TRIO_C.
DR InterPro: IPR008273; CRAL_TRIO_N.
DR InterPro: IPR000348; Emp24_gp25L_p24.
DR InterPro: IPR009038; GOLD.
DR InterPro: IPR001071; Retbind/tocTrans.
DR Pfam; PF00650; CRAL_TRIO; 1.
DR Pfam; PF03765; CRAL_TRIO_N; 1.
DR Pfam; PF01105; EMP24_GP25L; 1.
DR PRINTS; PR00180; CRETINALDHP.
DR SMART; SM00516; SEC14; 1.
DR PROSITE; PS00191; CRAL_TRIO; 1.
DR PROSITE; PS00866; GOLD; 1.
DR SEQUENCE 401 AA; 46084 MW; 704A92A72F82FB57 CRC64;

Query Match 69.8%; Score 1408.5; DB 2; Length 401;
Best Local Similarity 66.0%; Pred. No. 3.8e-106;
Matches 266; Conservative 51; Mismatches 57; Indels 29; Gaps 5;

QY 1 MSGRVGDLSPROKEALAK-----PEASTCSRSPRRCGSGMWSSES----- 39
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QY 40 --KRTLTTS--LAWQPEVIQOYLGGMCGYDLDCPWWYDIIGPKDAKGLLFSASKODL 95
DB 61 EFRKTMIDHLDHQPEVIQYKMPGGLCGYDRDGCPCWYDIIGPLPKGLLFSVTKODL 120

QY 96 LRTKMRCELLQECAGHTTKLGRKVTITIIYDCGGLGLKHLWKPAVEAYGEFLCMFEE 155
DB 121 LKTRMDCERILHECDLQTERLGRKTIETIIVIFDCGGLGLKHLWKPAVEAYGEFLLEE 180

QY 156 NYPETLKLFLVWAKPLFPVAYNLIKPFLSDTRKKIMVLGAN-YKEVLLKHISPDQVVP 214
DB 181 NYPETLKPMLIVKATKLPFGVGNLMPFLSDTRRKIVVLGNSWKEGLLKLIPEELPA 240

QY 215 YGGTMTDPDGNPKCKSKINYGDIIPRKYIVRDQVKQYEHVSQISRGSSHQVEYELLFPP 274
DB 241 HFGGTLTDPDGNPKCLTKINYGGEIPKSMYVRDQVKQYEHVSQISRGSSHQVEYELLFPP 300

QY 275 GCVLRWQFSSGDADVGFGIFLTKMGERQKAGEMTEVLVLPNQRVNSHLVPEDGTLTCSDPG 334
DB 301 GCVLRWQFSSGDADIGFVFLTKMGERQKAGEMTEVLTSQRYNAHVPEDGSLTCSAG 360

QY 335 IYVLRPDNTYSFIHAKKNFTVEVLLPDKASEKMKQLGAGTP 377

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Job time : 235 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Perfect score: 2018
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Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1272	63.0	391	2	US-10-104-047-2798
2	1118	55.4	360	2	US-10-104-047-3609
3	394	19.5	723	2	US-09-949-016-9810
4	344.5	17.1	308	2	US-09-270-767-33202
5	344.5	17.1	308	2	US-09-270-767-48419
6	197	9.8	304	2	US-09-538-092-613
7	181.5	9.0	293	2	US-09-248-796A-18524
8	181	9.0	278	2	US-08-557-614-2
9	181	9.0	278	2	US-08-557-614-23
10	144	7.1	330	2	US-09-270-767-43290
11	124	6.1	301	2	US-09-270-767-43653
12	115.5	5.7	341	2	US-09-244-805-61
13	114.5	5.7	136	2	US-09-270-767-32985
14	114.5	5.7	136	2	US-09-270-767-48202
15	113	5.6	342	2	US-09-244-805-62378
16	111	5.5	316	2	US-09-270-767-43378
17	111	5.5	778	2	US-09-270-767-45008
18	110	5.5	317	2	US-09-949-016-5927
19	110	5.5	344	2	US-09-949-016-9647
20	110	5.5	433	2	US-09-507-765-30
21	110	5.5	433	2	US-09-507-765-31
22	109	5.4	274	2	US-09-270-767-32136
23	109	5.4	274	2	US-09-270-767-47353
24	109	5.4	823	2	US-09-270-767-42450
25	107	5.3	135	2	US-09-270-767-58728
26	107	5.3	135	2	US-09-270-767-60491
27	107	5.3	342	2	US-09-248-796A-15115

28	105.5	5.2	108	2	US-09-270-767-59035	Sequence 59035, A
29	102	5.1	433	2	US-09-248-796A-18046	Sequence 18046, A
30	100.5	5.0	319	2	US-09-270-767-32632	Sequence 32632, A
31	100.5	5.0	319	2	US-09-270-767-47849	Sequence 47849, A
32	98.5	4.9	736	1	US-08-788-892-2	Sequence 2, Appli
33	98.5	4.9	736	1	US-09-340-475-2	Sequence 2, Appli
34	97	4.8	341	1	US-08-530-566-7	Sequence 7, Appli
35	97	4.8	341	2	US-09-195-728-7	Sequence 7, Appli
36	97	4.8	341	2	US-09-067-755-7	Sequence 9, Appli
37	95	4.7	341	1	US-08-530-566-9	Sequence 9, Appli
38	95	4.7	341	2	US-09-195-726-9	Sequence 9, Appli
39	95	4.7	341	2	US-09-067-755-9	Sequence 3753, Ap
40	95	4.7	418	2	US-09-134-001C-3753	Sequence 37, Appl
41	95	4.7	1440	2	US-09-357-251-37	Sequence 3655, Ap
42	94	4.7	736	2	US-09-134-001C-3655	Sequence 10, Appl
43	94	4.7	762	1	US-08-907-166-10	Sequence 10, Appl
44	94	4.7	762	2	US-09-391-340-10	Sequence 4, Appli
45	93	4.6	593	1	US-08-900-927-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-104-047-2798
; Sequence 2798, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2798
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2798

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Qy	64	CGYDLGCPWYDI	IIGPKDAKGLLFSASKODLARTKWR	CELLLOECAHOTTKLGR	KVET	123
Db	74	CGYDEGCPYFNI	IIGSLDPKGLLSASKODMIRKRIK	VCCELLHCELOTKLGR	KIEM	133
Qy	124	ITTIYCEGGLKHL	KWPAVEAYGEFLCMFEENYPETL	KRLFFVVKAPKLPFV	AVNLIKPF	183
Db	134	ALIVFDNEGSL	KHLWKPAVEVYQQFPILEANYPET	LKNLIVIRAPKLPFV	APNVLKSF	193
Qy	184	LSBDRKKIMVL	GANYKEVLLKHISPDQVPEVGGT	WTDPDGPNPKSKSKIN	YGGDIPRKY	243
Db	194	MSEETRKRKIV	LGDNWKQELTKFISPDQLPVEFG	TWTDPDGPNPKCLTKI	NYGGEVPSY	253
Qy	244	YVRDQVQOYEH	SVQISRGSSHQVEIILPFGCVLR	WQFMSDGDVCGFIFL	KTMMGERQ	303
Db	254	YLCEQVRLQY	EHTRSVGRSSLOVENEILPFGC	VLRWQFASDGGDIDG	FVFLKTMGEQQ	313
Qy	304	RAGMTVELPN	ORNSHLVPEDGTLTCSDPGIYV	LRFDNTYSFTHAKKVN	FTVLLPDK	363
Db	314	SAREMTVELP	SQRNAHNVFEDGSLTCLQAGV	YVLRFDNTYSRMVAK	LSYTVVLLPDK	373
Qy	364	ASEEKMQLG	AGTGP	377		
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Db 374 ASEETLQSLKAWRP 387

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US-10-104-047-3609
; Sequence 3609, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3609
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3609

Query Match      55.4%; Score 1118; DB 2: Length 360;
Best Local Similarity 66.1%; Pred. No. 1.9e-120;
Matches 197; Conservative 49; Mismatches 52; Indels 0; Gaps 0;

Qy 40 KRTLTTSLAWQPVEIQYLSGGMCGYDLDGCPVWYDIIGPKDAKGILFSASKQDLRLTK 99
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Db 11 QQDLNIVTWQPPEVIQLYDSGLCGDYEGCVPVENIIGSLDPKGLILLSASKQDMIRKR 70

Qy 100 MRECELLLOECAHQTTLGRKVETITIIYDCGELGLXHLWKPAVEAYGBFLCMFEENYPE 159
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Qy 160 TLKRLFVVKAPKLPFAVNLIKPFLESDETRKKIMVLGANLYKEVLLKHISPDQVPVEYGCT 219
    |||||:: |||||:: |||||:: |||||:: |||||:: |||||:: |||||:: |||||:: |||||:
Db 131 TLKNLVIRAPKLPFAVNLVKSFMSEBTRKIVILGNWKQELTFEISPDQLPVEFGGT 190

Qy 220 MTDPDGNPKCKSKINYGDDIPRKYVRDQVKQOYEHSVOISRGSSHQVEYELLFPQCVLR 279
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Db 251 WQFASDGDIGFVGLFKTQMGEQQSAREMTEVLPSQRNAHVMPEDGSILTCLQAGYVV 308


RESULT 3
US-09-949-016-9810
; Sequence 9810, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9810
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9810
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Query Match 7.1%; Score 144; DB 2; Length 330;
Best Local Similarity 26.4%; Pred. No. 1.3e-07;

Matches 48; Conservative 27; Mismatches 53; Indels 54; Gaps 7;
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Db 121 LKYGACENIIPSKLRNVFEANTILNLPQDQGRRLLVLEAGKWKQSPQVPLVDFRGI 180
QY 113 QTTKLGRKVTIT-----IYDCGLGLKHL--WKPAVEA-----YGBFLCMFEENYPE 159
Db 181 QLTVLGSMVEPPSQIGSVVIMDEGLPLSHITQTFPSFAAMLLDVIQECIM----- 233
QY 160 TLKRLFFVKAPKLPFVAYNLKIPFLSEDTTRKKIMVLGANYKEVLLKHISPDQVPVYGGT 219
Db 234 RLKAVHVNNSYIFNMLFAVKFFIREKLKRIFFGKDKYS-LISHIEAKALPPKYGGS 292
QY 220 MT 221
Db 293 AT 294

RESULT 11
US-09-270-767-43653
; Sequence 43653, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43653
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43653

Query Match 6.1%; Score 124; DB 2; Length 301;
Best Local Similarity 22.2%; Pred. No. 2.4e-05;
Matches 41; Conservative 31; Mismatches 71; Indels 42; Gaps 6;
QY 84 KGLLFSASKQDRLR-----TKMRECE-----LLQEC-----AHQT 114
Db 103 RGLLVEQKEKFKVKGSVINLVKNCQKGRVLIVNCCKLWDPSDITSDMFRLMYVHLA 162
QY 115 TLKGR--KVETITIIYDCGLGLKHLWKPAVEAYGEFLCMFEENYPETLKLFLVVKAPKL 172
Db 163 AQLSEETQVRGVVCIIMDFEGLSMKQKALSPSPSKRLLTFTQEAMPLRMKEVHFVKQFFI 222
QY 173 FPVAYNLKIPFLSEDTTRKKIMVLGANYKEVLLKHISPDQVPVYGGTMTDGNPKCKSK 232
Db 223 FNMVWSLFPKPVKQLNRMHFHGDMSKS-LQKFLDPSVLFPANYKGTL-----PA 271
QY 233 INYGG 237
Db 272 IDYGG 276

RESULT 12
US-09-244-805-61
; Sequence 61, Application US/09244805
; Patent No. 6699660
; GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimisch, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; THEREFOR

; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(341)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-244-805-61

Query Match 5.7%; Score 115.5; DB 2; Length 341;
Best Local Similarity 22.5%; Pred. No. 0.00029;
Matches 50; Conservative 36; Mismatches 85; Indels 51; Gaps 9;
QY 43 LTTSLAWQPPEVIQVLSGCMGYD-----LDGC-----PWYDIIGPKDAKGLLFS 90
Db 73 LSTSL---DDAFLRLFRARKFDYDRALQLLVNHYGCRSRWPEVFNLRPSALKDVLNSG 129
QY 91 SKQDLRLTKMRECELL-----LQSCAHTTKLGRKVT-----ITIIYD 129
Db 130 FLTVLPHTPRGCHVLCIRPDWIPSNYPITENIRAIYLTLEKLIQSEETQVNGVILAD 189
QY 130 CEGIGLKLWKPAVEAYGEFLC-----MFEENYPETLKLFLVVKAPKLPVAYNLKIPFL 184
Db 190 YKGVSL-----KASHFGPIARKVIGILQDGFPPIKAVHIVNEPRFKGIFAIKPF 244
QY 185 SEDTRKKIMVLGANYKEVLLKHISPDQ---VPVEYGGTMTDPD 224
Db .245 KEKIANRFFLHSGDLSL---HTSLPRNLPKEYGGTAGELD 283

RESULT 13
US-09-270-767-32985
; Sequence 32985, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32985
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32985

Query Match 5.7%; Score 114.5; DB 2; Length 136;
Best Local Similarity 24.6%; Pred. No. 8e-05;
Matches 33; Conservative 35; Mismatches 49; Indels 17; Gaps 6;
QY 240 PRKYVYRDQVKQYEH---SVOISRGSSHOVEYEI-LFPGCVLRQWQMSDCAVGFJF- 294
Db 1 PEELYI-DQSSQSDRDFVEAQVPGDKLKLHFKVWVEEQKILSWERTDYDIKFGIYS 59
QY 295 LKTKWGERQAGEMTEVLPNQVNSHLVPEDGTLCSDPGIYVLRPONTYSFTHAKKNF 354
Db 60 VDDKTGKRSEVPVLTGYVNE-----MDEIGYISTRPTNTYTVVFDNSASLYRSKKLRY 113
QY 355 TVEVLLPDKASEEK 368
Db 114 WVDLI-----SEEE 122

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 18:49:42 ; Search time 165 Seconds
(without alignments)
957.209 Million cell updates/sec

Title: US-10-696-699A-2
Perfect score: 2018
Sequence: 1 MSRGVGLSPRQKALAKPE.....LLPDKASEKKQLGAGTPK 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	378	4	US-10-419-629-2
2	2018	100.0	378	4	US-10-696-699A-2
3	1827.5	90.6	403	4	US-10-220-475A-4
4	1827.5	90.6	403	4	US-10-419-629-4
5	1827.5	90.6	403	4	US-10-072-012-448
6	1827.5	90.6	403	4	US-10-696-699A-4
7	1827.5	90.6	403	5	US-10-723-860-1875
8	1827.5	90.6	403	5	US-10-732-923-22953
9	1827.5	90.6	403	5	US-10-732-923-22954
10	1827.5	90.6	403	5	US-10-631-467-841
11	1827.5	90.6	403	5	US-10-745-237-294
12	1724.5	85.5	403	4	US-10-072-012-450
13	1724.5	85.5	403	5	US-10-732-923-22957
14	1724.5	85.4	403	4	US-10-220-475A-2
15	1722.5	85.4	403	4	US-10-072-012-449
16	1722.5	85.4	403	5	US-10-732-923-22778
17	1685.5	83.5	403	5	US-10-732-923-22958
18	1616.5	80.1	387	5	US-10-732-923-22957
19	1548	76.7	293	4	US-10-696-699A-15
20	1428	70.8	400	4	US-10-220-475A-17
21	1428	70.8	400	5	US-10-732-923-22956
22	1423.5	70.5	419	5	US-10-450-763-43464
23	1413	70.0	400	4	US-10-072-012-451
24	1413	70.0	400	5	US-10-732-923-22780
25	1309.5	64.9	403	5	US-10-732-923-22774
26	1304.5	64.6	406	4	US-10-220-475A-18
27	1304.5	64.6	406	4	US-10-072-012-447

28	1304.5	64.6	406	5	US-10-732-923-22950
29	1272	63.0	391	4	US-10-104-047-2798
30	1254	62.1	416	4	US-10-072-012-124
31	1227.5	60.8	415	4	US-10-072-012-122
32	1200.5	59.5	502	5	US-10-450-763-43046
33	1194	59.2	226	4	US-10-696-699A-17
34	1148.5	56.9	405	4	US-10-072-012-126
35	1118	55.4	360	4	US-10-104-047-3609
36	809	40.1	300	4	US-10-336-472-46
37	804	39.8	151	4	US-10-696-699A-19
38	752	37.3	240	5	US-10-450-763-43044
39	689	34.1	268	4	US-10-336-472-48
40	661.5	32.8	343	5	US-10-732-923-22946
41	518	25.7	385	5	US-10-732-923-22959
42	439	21.8	407	5	US-10-732-923-22977
43	439	21.8	407	5	US-10-745-237-100
44	435	21.6	385	6	US-11-097-143-33039
45	433	21.5	696	4	US-10-478-245-6

ALIGNMENTS

RESULT 1

US-10-419-629-2
; Sequence 2, Application US/10419629
; Publication No. US20040023915A1
; GENERAL INFORMATION:
; APPLICANT: Sanders, Bob G.
; APPLICANT: Kline, Kimberly
; APPLICANT: Yu, Weiping
; APPLICANT: Liu, Hui
; APPLICANT: Hantash, Feras
; TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
; FILE REFERENCE: D6453
; CURRENT APPLICATION NUMBER: US/10/419,629
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US 60/373,870
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: P2P polypeptide
US-10-419-629-2

Query Match	100.0%;	Score 2018;	DB 4;	Length 378;
Best Local Similarity	100.0%;	Pred. No. 8.e-194;		
Matches 378;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MSRGVGLSPRQKALAKPEASTCRSRPCSGMWSSESKRTLTTS	LAWPPEVIQYLS	60
Db	1	MSRGVGLSPRQKALAKPEASTCRSRPCSGMWSSESKRTLTTS	LAWPPEVIQYLS	60
QY	61	GMCGVDLDCGPVWYDIIGPKDAKGLLFSASKODLLATKRECELLI	LOECAHQTTKLRK	120
Db	61	GMCGVDLDCGPVWYDIIGPKDAKGLLFSASKODLLATKRECELLI	LOECAHQTTKLRK	120
QY	121	VEITIIYDCGGLGKHLWKPAAVEAYGEFLCMPEENYPETLKR	LVVVKAPKLPVAVNLI	180
Db	121	VEITIIYDCGGLGKHLWKPAAVEAYGEFLCMPEENYPETLKR	LVVVKAPKLPVAVNLI	180
QY	181	KPFLSEDTTRKKIWLGNANYKEVLKHLISPDQVPVEYGGTMTD	PDGPNPKCKSKINYGDI	240
Db	181	KPFLSEDTTRKKIWLGNANYKEVLKHLISPDQVPVEYGGTMTD	PDGPNPKCKSKINYGDI	240
QY	241	RKYVVRDQVKKQVEHSHVQISRGSSHQVEYIELPFGCVLRWQF	MSDGDADVGFI	300
Db	241	RKYVVRDQVKKQVEHSHVQISRGSSHQVEYIELPFGCVLRWQF	MSDGDADVGFI	300


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; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: TAP-46 polypeptide
; US-10-419-629-4

Query Match          90.6%; Score 1827.5; DB 4; Length 403;
Best Local Similarity 87.1%; Pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

Qy 1 MSGRVGDLSPRQKALAK-----PEASTCRSRRCSSGMWSES----- 39
Db 1 MSGRVGDLSPRQKALAKFRENVQDLPALPNPDYFLRLWLRLARSFDLQKSEAMLRKHV 60
Qy 40 ----KRTLTITTSLSAWQPPPIVQOYLISGGMCGYDLGCPWYDIILGPKDAKGLLFSASKQDL 95
Db 61 EFRKQKOIDNIISWQPPPIVQOYLISGGMCGYDLGCPWYDIILGPKDAKGLLFSASKQDL 120
Qy 96 LRTKWRCELLLQECASHQTTKLGKRKVEITITIIYDCEGLGLKHLWKPKAVEAYGEFLCMPEE 155
Db 121 LRTKWRCELLLQECASHQTTKLGKRKVEITITIIYDCEGLGLKHLWKPKAVEAYGEFLCMPEE 180
Qy 156 NYPETLKRLLFVVKAPKLPVAYNLIKPPLSEDTKKIMVLGANYKEVILLKHISPDQVPE 215
Db 181 NYPETLKRLLFVVKAPKLPVAYNLIKPPLSEDTKKIMVLGANYKEVILLKHISPDQVPE 240
Qy 216 YGGTWTDPDGNPKCKSKINYGGDIPRKYYVRDQVKQVEHSVQISRGSSHQVEYIILFPG 275
Db 241 YGGTWTDPDGNPKCKSKINYGGDIPRKYYVRDQVKQVEHSVQISRGSSHQVEYIILFPG 300
Qy 276 CVLRWQFMSDCADVGFGLFKLTQWGERORAGEMTEVLPNQRYNSHLVPEDEGTLTCSDPGI 335
Db 301 CVLRWQFMSDCADVGFGLFKLTQWGERORAGEMTEVLPNQRYNSHLVPEDEGTLTCSDPGI 360
Qy 336 YVLRFDNTYSFIHAKKNFTVEVLLPDKASBEKKMQLGAGTPK 378
Db 361 YVLRFDNTYSFIHAKKNFTVEVLLPDKASBEKKMQLGAGTPK 403

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RESULT 5
US-10-072-012-448
; Sequence 448, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shmukets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514

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; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 448
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-012-448

Query Match          90.6%; Score 1827.5; DB 4; Length 403;
Best Local Similarity 87.1%; Pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2

Qy      1 MSGRVGDLSPRQKEALAK-----PEASTCSRRRPCSGSMWSSES----- 39
        |||.....|||
Db      1 MSGRVGDLSPRQKEALAKFRENVDVLPAFPDDYFLLRWLRLARSFDLQKSEAMLRKHV 60
        |||.....|||

Qy      40 ----KPTLTTSLLAWOPPEVIQQYLSCGCGYDLDGCPWYDIIGPKDAKGLLFSASKODL 95
        :::::|||||
Db      61 EFRQKDIDNIISQPPEVIQQYLSCGCGYDLDGCPWYDIIGPLDKAGLLFSASKODL 120
        :::::|||||

Qy      96 LRTQWRCELLQLQBCAHTTKLGKRKVETITIIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 155
        |||.....|||
Db      121 LRTQWRCELLQLQBCAHTTKLGKRKVETITIIYDCEGLGLKHLWKPAVEAYGEFLCMFEE 180
        |||.....|||

Qy      156 NYPETLKRLFVKAPKLFPVAYNLIKPFSLSDTRKKIMVLGCANYKEVULLKHISPQDVPE 215
        |||.....|||
Db      181 NYPETLKRLFVKAPKLFPVAYNLIKPFSLSDTRKKIMVLGCANYKEVULLKHISPQDVPE 240
        |||.....|||

Qy      216 YGGTMTDPDGNPKCKSKINYGDDIPRKYYVRDQVKQYEHVSVOISRGSSSHQVEYIILPFG 275
        |||.....|||
Db      241 YGGTMTDPDGNPKCKSKINYGDDIPRKYYVRDQVKQYEHVSVOISRGSSSHQVEYIILPFG 300
        |||.....|||

Qy      276 CVLRQWFMSDGDADVGFGLFKTKMGQRQAGEMTEVLPNQRYNSHLPVEDGTTLTCSDPGI 335
        |||.....|||
Db      301 CVLRQWFMSDGDADVGFGLFKTKMGQRQAGEMTEVLPNQRYNSHLPVEDGTTLTCSDPGI 360
        |||.....|||

Qy      336 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKMQLGAGTPK 378
        |||.....|||
Db      361 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKMQLGAGTPK 403
        |||.....|||

RESULT 6
US-10-696-699A-4
; Sequence 4, Application US/10696699A
; Publication No. US20040152883A1
; GENERAL INFORMATION:
; APPLICANT: Sanders, Bob G.
; APPLICANT: Kline, Kimberly
; APPLICANT: Yu, Weiping
; APPLICANT: Liu, Hui
; APPLICANT: Hantaesh, Feras
; TITLE OF INVENTION: Tocopherol Associated Protein and Uses Thereof
; FILE REFERENCE: D6453CIP
; CURRENT APPLICATION NUMBER: US/10/696,699A
; CURRENT FILING DATE: 2003-10-29
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Query Match      90.6%; Score 1827.5; DB 5; Length 403;
Best Local Similarity 87.1%; pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

OV 1 MSRGVGLSPROKEALAK-----PEASTCRSRRCGSMWSSSES----- 39

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Query Match	90.6%	Score	1827.5	DB	5	Length	403
Best Local Similarity	87.1%	Pred. No.	1.4e-174				
Matches	351	Conservative	9	Mismatches	18	Indels	25
Gap							
Qy	1	MSGRVGDLS	SPRQKEALAK	-----	PEASTCRSRRCPSGSMWSSS	-----	39
Db	1	MSGRVGDLS	SPRQKEALAK	PFRENVQDVL	PALPNDDHFLRLWLRARS	FDLQKSEAML	RKHV 60
Qy	40	-----	KRTLTSLAWQ	PPEVTQQYLS	SGMCGYDLDG	CPVWYDIITG	PKDAKGLLFP
Db	61	EFKQKQIDNII	ISWQPPEVTQQYLS	SGMCGYDLDG	CPVWYDIITG	PLDAKGLLFP	SASKQDL 120
Qy	96	LRTKMRCE	LLQBCAHQTTK	LRGKVEVTITII	YDCEGLGLKHL	WKPAVEAYG	EFLCFMFE 155
Db	121	LRTKMRCE	LLQBCAHQTTK	LRGKVEVTITII	YDCEGLGLKHL	WKPAVEAYG	EFLCFMFE 180
Qy	156	NYPETL	KRLFVW	KAPLFP	VAYNLIRPF	LSEDTRKKIMV	GANYKEVLLKHIS
Db	181	NYPETL	KRLFVW	KAPLFP	VAYNLIRPF	LSEDTRKKIMV	GANYKEVLLKHIS
Qy	216	YGGTMTD	PDGNPKCKS	KINTGGDI	PRKYVYRDQ	VQKQYEH	SVQISRGSSSHOVE
Db	241	YGGTMTD	PDGNPKCKS	KINTGGDI	PRKYVYRDQ	VQKQYEH	SVQISRGSSSHOVE
Qy	276	CVLRWQ	PMSD	GDVGG	GFIFLTKTK	GRQAGE	TEVLPNQRYNSHLV
							PDGTLTCS
							DPGI 335

Db 301 CVLRWQFMSDGDVGFGLFKTKMGERORAGEMTEVLPNORYNSHLVDPDGTLTCSDPGI 360
QY 336 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 378
Db 361 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 403

RESULT 9

US-10-732-923-22954
; Sequence 22954, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22954
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-22954

Query Match 90.6%; Score 1827.5; DB 5; Length 403;
Best Local Similarity 87.1%; Pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

QY 1 MSGRVGDLSPROKEALAK-----PEASTCRSRPPCGSGMSSS----- 39
Db 1 MSGRVGDLSPROKEALAKFRENVDVLPALPNPDDYFLLRWLRARSPDLQKSEAMLRKHV 60
QY 40 ----KRTLTTSLAWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL 95
Db 61 EPRKQKIDNIISWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL 120
QY 96 LRTKRECELLQECACHOTTKLGRKVETITIIYDCGELGLKHLWKPAVEAYGEFLCMFEE 155
Db 121 LRTKRECELLQECACHOTTKLGRKVETITIIYDCGELGLKHLWKPAVEAYGEFLCMFEE 180
QY 156 NYPETLRLFWVKAPKLPVAVYNLIKPFLESDTRKKIMVLGANYKEYLLKHISPDQVPVE 215
Db 181 NYPETLRLFWVKAPKLPVAVYNLIKPFLESDTRKKIMVLGANYKEYLLKHISPDQVPVE 240
QY 216 YGGTMTDPGNPKCKSKINYGDIIPRKYVVRDQVKQYEHVSQISRGSSHQVEYIELPPG 275
Db 241 YGGTMTDPGNPKCKSKINYGDIIPRKYVVRDQVKQYEHVSQISRGSSHQVEYIELPPG 300
QY 276 CVLRWQFMSDGDVGFGLFKTKMGERORAGEMTEVLPNORYNSHLVDPDGTLTCSDPGI 335
Db 301 CVLRWQFMSDGDVGFGLFKTKMGERORAGEMTEVLPNORYNSHLVDPDGTLTCSDPGI 360
QY 336 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 378
Db 361 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 403

RESULT 10

US-10-631-467-841
; Sequence 841, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive P
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312

; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 841
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-841

Query Match 90.6%; Score 1827.5; DB 5; Length 403;
Best Local Similarity 87.1%; Pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

QY 1 MSGRVGDLSPROKEALAK-----PEASTCRSRPPCGSGMSSS----- 39
Db 1 MSGRVGDLSPROKEALAKFRENVDVLPALPNPDDYFLLRWLRARSPDLQKSEAMLRKHV 60
QY 40 ----KRTLTTSLAWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL 95
Db 61 EPRKQKIDNIISWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL 120
QY 96 LRTKRECELLQECACHOTTKLGRKVETITIIYDCGELGLKHLWKPAVEAYGEFLCMFEE 155
Db 121 LRTKRECELLQECACHOTTKLGRKVETITIIYDCGELGLKHLWKPAVEAYGEFLCMFEE 180
QY 156 NYPETLRLFWVKAPKLPVAVYNLIKPFLESDTRKKIMVLGANYKEYLLKHISPDQVPVE 215
Db 181 NYPETLRLFWVKAPKLPVAVYNLIKPFLESDTRKKIMVLGANYKEYLLKHISPDQVPVE 240
QY 216 YGGTMTDPGNPKCKSKINYGDIIPRKYVVRDQVKQYEHVSQISRGSSHQVEYIELPPG 275
Db 241 YGGTMTDPGNPKCKSKINYGDIIPRKYVVRDQVKQYEHVSQISRGSSHQVEYIELPPG 300
QY 276 CVLRWQFMSDGDVGFGLFKTKMGERORAGEMTEVLPNORYNSHLVDPDGTLTCSDPGI 335
Db 301 CVLRWQFMSDGDVGFGLFKTKMGERORAGEMTEVLPNORYNSHLVDPDGTLTCSDPGI 360
QY 336 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 378
Db 361 YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK 403

RESULT 11

US-10-745-237-294
; Sequence 294, Application US/10745237
; Publication No. US20050227301A1
; GENERAL INFORMATION:
; APPLICANT: Cyclacel Limited
; APPLICANT: Glover, David
; APPLICANT: Bell, Graham
; APPLICANT: Frenz, Lisa
; APPLICANT: Midgley, Carol
; TITLE OF INVENTION: Cell Cycle Progression Proteins
; FILE REFERENCE: P0158190 CVK
; CURRENT APPLICATION NUMBER: US/10/745,237
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/439,123
; PRIOR FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/468,402
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 294
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 076054
US-10-745-237-294

Query Match 90.6%; Score 1827.5; DB 5; Length 403;
Best Local Similarity 87.1%; Pred. No. 1.4e-174;
Matches 351; Conservative 9; Mismatches 18; Indels 25; Gaps 2;

QY 1 MSRGVGDLSPRQKEALAK-----PEASTCSRPPCSGSMWSSES----- 39
DB 1 MSRGVGDLSPRQKEALAKFRENVDVLPPLPNDPDDYFLRLWRARSFDLQKSEAMLRKHV 60
QY 40 ----KRTLTTSIAWQPPEVIQQYLSGCMCGYDLGCPVWYDIIGPKDAKGLLFSASKQDL 95
DB 61 EFRKQKDIKIISWQPPEVIQQYLSGRCGYDLGCPVWYDIIGPLDAKGLLFSASKQDL 120
QY 96 LRTKMRCELLQCEAHQTTKLGKRVETITIIYDCGSLGLKHLWKPAVEAYGEFLTMFEE 155
DB 121 LRTKMRDCCELLQCEIQTTQTKLGKIKETITMIYDCGSLGLKHLWKPAVEAYGEFLTMFEE 180
QY 156 NYPETLKRLLFVVKAPKLPVAYNLIKPFVSEDRKKIMVLGANYKEVLLKHLSPDQPVPE 215
DB 181 NYPETLKRLLFVVKAPKLPVAYNLIKPFVSEDRKKIMVLGANYKEVLLKHLSPDQPVPE 240
QY 216 YGGTMTDPDGNPKCKSKINYGGDIIPKQYVVRDQVKKQYEHVSQISRGSSHQVEYELFPFG 275
DB 241 YGGTMTDPDGNPKCKSKINYGGDIIPKQYVVRDQVKKQYEHVTQVSRGSSHQVEYELFPFG 300
QY 276 CVLRWQFMSGDADVGFGLFKTKMGERQORAGEMTEVLPNQRVNSHLVPEDEGTLTCSDPGI 335
DB 301 CVLRWQFMSGSDVGFGLFKTKMGERQORAGEMTEVLPNQRVNSHVMVPEDEGTLTCSPEGI 360
QY 336 YVLRFDNTYSFIHAKKNVFTVEVLLPDKASEEKKQLGAGTPK 378
DB 361 YVLRFDNTYSFIHAKKVSFTVEVLLPDKAAEEKLNQOQNAVTPK 403

RESULT 14
US-10-220-475A-2
; Sequence 2, Application US/10220475A
; Publication No. US20040023227A1
; GENERAL INFORMATION:
; APPLICANT: INQUE, KEIZO
; APPLICANT: ARAI, HIROYUKI
; APPLICANT: ARITA, MAKOTO
; TITLE OF INVENTION: DNA ENCODING SQUALENE EPOXIDASE-PROMOTING FACTOR
; FILE REFERENCE: 04853.0096-00000
; CURRENT APPLICATION NUMBER: US/10/220,475A
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: PCT/JP01/01592
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: JP 2000-57743
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-220-475A-2

Query Match 85.4%; Score 1722.5; DB 4; Length 403;
Best Local Similarity 81.1%; Pred. No. 5.2e-164;
Matches 327; Conservative 25; Mismatches 26; Indels 25; Gaps 2;

QY 1 MSRGVGDLSPRQKEALAK-----PEASTCSRPPCSGSMWSSES----- 39
DB 1 MSRGVGDLSPRQKEALAKFRENVDVLPALPNPDDYFLRLWRARSFDLQKSEAMLRKHV 60
QY 40 ----KRTLTTSIAWQPPEVIQQYLSGCMCGYDLGCPVWYDIIGPKDAKGLLFSASKQDL 95
DB 61 EFRKQKDIKIISWQPPEVIQQYLSGRCGYDLGCPVWYDIIGPLDAKGLLFSASKQDL 120
QY 96 LRTKMRCELLQCEAHQTTKLGKRVETITIIYDCGSLGLKHLWKPAVEAYGEFLTMFEE 155
DB 121 LRTKMRDCCELLQCEIQTTQTKLGKIKETITMIYDCGSLGLKHLWKPAVEAYGEFLTMFEE 180
QY 156 NYPETLKRLLFVVKAPKLPVAYNLIKPFVSEDRKKIMVLGANYKEVLLKHLSPDQPVPE 215
DB 181 NYPETLKRLLFVVKAPKLPVAYNLIKPFVSEDRKKIMVLGANYKEVLLKHLSPDQPVPE 240

QY 216 YGGTMTDPDGNPKCKSKINYGGDIIPKQYVVRDQVKKQYEHVSQISRGSSHQVEYELFPFG 275
DB 241 YGGTMTDPDGNPKCKSKINYGGDIIPKQYVVRDQVKKQYEHVSQISRGSSHQVEYELFPFG 300
QY 276 CVLRWQFMSGDADVGFGLFKTKMGERQORAGEMTEVLPNQRVNSHLVPEDEGTLTCSDPGI 335
DB 301 CVLRWQFMSGSDVGFGLFKTKMGERQORAGEMTEVLPNQRVNSHVMVPEDEGTLTCSPEGI 360
QY 336 YVLRFDNTYSFIHAKKNVFTVEVLLPDKASEEKKQLGAGTPK 378
DB 361 YVLRFDNTYSFIHAKKVSFTVEVLLPDKAAEEKLNQOQNAVTPK 403
RESULT 15
US-10-072-012-449
; Sequence 449, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Fatturajan, Meera
; APPLICANT: Shimkete, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Molenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsebrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 449
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Rattus norvegicus

US-10-072-012-449

Query Match	85.4%	Score	1722.5	DB	4	Length	403		
Best Local Similarity	81.1%	Pred. No.	5.2e-164						
Matches	327	Conservative	25	Mismatches	26	Indels	25	Gaps	2
Qy	1	MSGRVGDLSPQKEALAK-----PEASTCRSRRRCSCGSMWSSS-----	39						
Db	1	MSGRVGDLSPKQEEALAKFRNVQDVLPALEPNDDYFLLRWLRRSPDLQKSEAMLRKHV	60						
Qy	40	-----KRTLTTSLEAWQPPEVIQQYLSGMCGYDLGCPVWYDIIGPKDAKGILLFSASKODL	95						
Db	61	EFRKQKIDKIISQWPPEVIQQYLSGRCRGYDLGCPVWYDIIGPLDAKGILLFSASKODL	120						
Qy	96	LRTKWRCELLQLQCAHOTTKLGKRVKFTITIIYDCEGLGLKHLWKPAVEAYGEFLCWFEE	155						
Db	121	LRTKWRCELLQLQECCTQATKLGKKIETITMIYDCEGLGLKHLWKPAVEAYGEFLTWEE	180						
Qy	156	NYPETLRLRFVVKAPKLPFVAYNALIKPFLSEDTTRKIMVLGANTKEYLLKXISPDPVPE	215						
Db	181	NYPETLRLRFVVKAPKLPFVAYNALIKPFLSEDTTRKIMVLGANKVEYLLKXISPQLPVE	240						
Qy	216	YGGTWTDPDGNPKCKSKINYGDDIPRKYYVRDQVKQYEHVSQVLSRGSSSHQVEYIILPPG	275						
Db	241	YGGTWTDPDGNPKCKSKINYGDDIPKQYYVRDQVKQYEHVSQVLSRGSSSHQVEYIILPPG	300						
Qy	276	CVLRWQFMSDCADVFGGIFLKTNGERQORAGEMTEVLPNQRYNSHLVPEDCGTLTCSDPGI	335						
Db	301	CVLRWQFMSSEGS DVFGGIFLKTNGERQORAGEMTEVLPNQRYNSHMWPEDCGTLTCSFPGI	360						
Qy	336	YVLRFDNTYSFIHAKKNFTVEVLLPKKASEBKWKQLGAGTPK	378						
Db	361	YVLRFDNTYSFIHAKKYSFTVEVLLPKKASEKLNQQCAVTPK	403						

Search completed: May 2, 2006, 18:53:26
Job time : 166 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 18:50:52 ; Search time 27 Seconds
(without alignments)
636.690 Million cell updates/sec

Title: US-10-696-699A-2
Perfect score: 2018
Sequence: 1 MSRGVGDLSPROKEALAKE.....LLPKASBEKMKQLGAGTPK 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 232119 seqs, 45477862 residues

Total number of hits satisfying chosen parameters: 232119

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep1:
2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep2:
3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep3:
4: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep4:
5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep5:
6: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep6:
7: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep7:
8: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep8:
9: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep9:
10: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep10:
11: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep11:
12: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1827.5	90.6	403	9	US-10-528-031-7
2	1272	63.0	391	11	US-11-072-512-2798
3	1118	55.4	360	11	US-11-072-512-3609
4	233	11.5	463	11	US-11-096-568A-7798
5	233	11.5	479	11	US-11-096-568A-7797
6	233	11.5	483	11	US-11-096-568A-7796
7	221.5	11.0	478	11	US-11-096-568A-28170
8	221.5	11.0	517	11	US-11-096-568A-28169
9	221.5	11.0	558	11	US-11-096-568A-28168
10	216	10.7	409	11	US-11-096-568A-32080
11	216	10.7	433	11	US-11-096-568A-32079
12	214	10.6	511	11	US-11-096-568A-27441
13	214	10.6	551	11	US-11-096-568A-27440
14	214	10.6	560	11	US-11-096-568A-27439
15	213	10.6	394	11	US-11-096-568A-9415
16	213	10.6	423	11	US-11-096-568A-9414
17	213	10.6	449	11	US-11-096-568A-9413
18	206	10.2	419	11	US-11-096-568A-26554
19	206	10.2	443	11	US-11-096-568A-26553
20	206	10.2	463	11	US-11-096-568A-18643
21	206	10.2	485	11	US-11-096-568A-26552

22	204	10.1	341	11	US-11-096-568A-32081	Sequence 32081, A
23	199.5	9.9	546	11	US-11-096-568A-27860	Sequence 27860, A
24	199.5	9.9	550	11	US-11-096-568A-27859	Sequence 27859, A
25	199.5	9.9	554	11	US-11-096-568A-27858	Sequence 27858, A
26	196	9.7	364	11	US-11-087-099-7476	Sequence 7476, Ap
27	193.5	9.6	313	11	US-11-096-568A-16949	Sequence 16949, A
28	193.5	9.6	520	11	US-11-096-568A-16948	Sequence 16948, A
29	186.5	9.2	302	11	US-11-087-099-6162	Sequence 6162, Ap
30	176.5	8.7	497	11	US-11-087-099-5884	Sequence 5884, Ap
31	176	8.7	137	11	US-11-096-568A-26460	Sequence 26460, A
32	176	8.7	156	11	US-11-096-568A-26459	Sequence 26459, A
33	173.5	8.6	430	11	US-11-096-568A-18644	Sequence 18644, A
34	158	7.8	247	11	US-11-087-099-5238	Sequence 5238, Ap
35	149	7.4	307	11	US-11-096-568A-18887	Sequence 18887, A
36	149	7.4	309	11	US-11-096-568A-18886	Sequence 18886, A
37	142.5	7.1	208	11	US-11-096-568A-13413	Sequence 13413, A
38	142.5	7.1	255	11	US-11-096-568A-13412	Sequence 13412, A
39	142.5	7.1	289	11	US-11-096-568A-13411	Sequence 13411, A
40	142	7.0	259	11	US-11-087-099-1922	Sequence 1922, Ap
41	141	7.0	254	11	US-11-087-099-10781	Sequence 10781, A
42	141	7.0	261	11	US-11-087-099-1647	Sequence 1647, Ap
43	140.5	7.0	255	11	US-11-087-099-308	Sequence 308, App
44	140	6.9	256	11	US-11-087-099-3617	Sequence 3617, Ap
45	140	6.9	256	11	US-11-087-099-10493	Sequence 10493, A

ALIGNMENTS

RESULT 1
US-10-528-031-7
; Sequence 7, Application US/10528031
; Publication No. US20050262577A1
; GENERAL INFORMATION:
; APPLICANT: ORIDIS BIOMED Forschungs- und Entwicklungs GmbH
; APPLICANT: Guelly, Christian
; APPLICANT: Buck, Charles R.
; APPLICANT: Zatloukal, Kurt
; TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for
; TITLE OF INVENTION: prevention, diagnosis or treatment of liver disorders and epith.
; FILE REFERENCE: Oridis Biomed
; CURRENT APPLICATION NUMBER: US/10/528,031
; CURRENT FILING DATE: 2005-03-16
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-528-031-7

Query Match	90.6%	Score 1827.5;	DB 9;	Length 403;
Best Local Similarity	87.1%	Pred. No. 1.3e-166;		
Matches 351;	Conservative	9;	Mismatches 18;	Indels 25; Gaps 2;
QY	1	MSRGVGDLSPROKEALAK-----PEASTCRSRRPCSGSMWSSS-----	39	
Db	1	MSRGVGDLSPROKEALAKFRENVDVLPALPNDDYFLRLWLRLARSFDLQKSEAMLRKHV	60	
QY	40	----KRTLTTSLAWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL	95	
Db	61	EPRKQKIDNIISWQPEVIQQYLSGCMGCGYLDGCPVWYDIIGPKDAKGLLFSASKQDL	120	
QY	96	LRTKMECELLLOECAHQTTLGRKVTETIIIVDCRGLGKHLWKPAVEAYGFLCMFEE	155	
Db	121	LRTKMECELLLOECAHQTTLGRKVTETIIIVDCRGLGKHLWKPAVEAYGFLCMFEE	180	
QY	156	NYPETLKLRFVVKAPKLPVAYNLIKPFLSEDRKKIMVLGANYKVELLKHISPDQVPVE	215	
Db	181	NYPETLKLRFVVKAPKLPVAYNLIKPFLSEDRKKIMVLGANYKVELLKHISPDQVPVE	240	
QY	216	YCGTMTDPCGNPKCKSKINYGDI PRKYVYRQVQKQYHSHVQISRGSSSHQVYEILFPG	275	

Db 241 YGGTWTDPDGNPKCKSKINYGGDI PRKYVVRDQVKKQYEHVSQISRGSSHQVEYBILFPG 300
QY 276 CVLRQFMSDGDADVGFGLFKTKMGERQAGTEVLNQRVNSHLVPEDGTLTCSDDGI 335
Db 301 CVLRQFMSDGDADVGFGLFKTKMGERQAGTEVLNQRVNSHLVPEDGTLTCSDDGI 360
QY 336 VYLRFDNTYSFTHAKKNFTVEVLPPDKASEEKMKGAGTGP 378
Db 361 VYLRFDNTYSFTHAKKNFTVEVLPPDKASEEKMKGAGTGP 403

RESULT 2

US-11-072-512-2798

; Sequence 2798, Application US/11072512

; Publication No. US20060029945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAOHIKO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOKYUKI

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: 084335-0191

; CURRENT APPLICATION NUMBER: US/11/072,512

; PRIOR FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/350,978

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: JP 2001-379298

; PRIOR FILING DATE: 2001-11-05

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2798

; LENGTH: 391

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-072-512-2798

Query Match 63.0%; Score 1272; DB 11; Length 391;
Best Local Similarity 62.0%; Pred. No. 1.7e-113;
Matches 232; Conservative 58; Mismatches 68; Indels 16; Gaps 2;

QY 20 EASTCRSRPCCSGS-----WMSSE--SKRTLTSLSLAWQPEVIQQVLSGGM 63
Db 14 ETLTCRNPKTSCGPKSPQPTSCPHALRAWHMFRKQDLDNIVTWQPEVTLQYDSGGL 73
QY 64 CGYDLDCGPVWDIIGPKDAKGLFSAKQDILLRTKMCRECELLLOECAHQTTLKGRKVET 123
Db 74 CGYDVEGCPVYFNIGSLDPKGLLSASKQDMIRKRVCELLHECELQTKGRKLEW 133
QY 124 ITIIVDCEGLGLKHLWKPAVEAYGEFLCMFEENYPTLKRLEFVVRAPKLPFVAYNLIRPF 183
Db 134 ALLVDFMEGLSKHLWKPAVEYVQQFFSILEANYPETLKNLIVIRAPKLPFVAFNLVKSF 193
QY 184 LSEDRKKIMVIGANYKEVLLKHHISPDQVPVEYGGTMDPDGNPKCKSKINYGGDI PRKY 243
Db 194 MSEETRRKIVILGDNWKQBELTKFISPDQLFVEFGGTMTPDGNPKCLTKINYGGEVPKSY 253
QY 244 VYRDQVKKQYEHVSQISRGSSHQVEYBILFPGCVLRWQFMSDGDADVGFGLFKTKMGERQ 303
Db 254 YLCEQVRLQYEHTRSVGRGSSLOVENEILLFPGCVLRWQFASDGGDVGFGVFLTKMGERQ 313

QY 304 RAGTEVLNQRVNSHLVPEDGTLTCSDDPGIYVLRFDNTYSFTHAKKNFTVEVLPPDK 363
Db 314 SAREMTEVLPSQRNAHMPEDGSLTCLQAGVYVLRFDNTYSRMYAKKLSTVEVLPPDK 373
QY 364 ASEEMKMKOLGAGTGP 377
Db 374 ASEETLQSLKAWRP 387

RESULT 3

US-11-072-512-3609

; Sequence 3609, Application US/11072512

; Publication No. US20060029945A1

; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU

; APPLICANT: OTSUKI, TETSUJI

; APPLICANT: WAKAMATSU, AI

; APPLICANT: SATO, HIROYUKI

; APPLICANT: ISHII, SHIZUKO

; APPLICANT: YAMAMOTO, JUN-ICHI

; APPLICANT: ISONO, YUUKO

; APPLICANT: HIO, YURI

; APPLICANT: OTSUKA, KAORU

; APPLICANT: NAGAI, KEIICHI

; APPLICANT: IRIE, RYOTARO

; APPLICANT: TAMECHIKA, ICHIRO

; APPLICANT: SEKI, NAOHIKO

; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOKYUKI

; APPLICANT: NAGAHARI, KENJI

; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: Novel full length cDNA

; FILE REFERENCE: 084335-0191

; CURRENT APPLICATION NUMBER: US/11/072,512

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: US 60/350,978

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: JP 2001-379298

; PRIOR FILING DATE: 2001-11-05

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3609

; LENGTH: 360

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-072-512-3609

Query Match 55.4%; Score 1118; DB 11; Length 360;
Best Local Similarity 66.1%; Pred. No. 7.9e-99;
Matches 197; Conservative 49; Mismatches 52; Indels 0; Gaps 0;

QY 40 KRTLTTSLAWQPEVIQQVLSGGMCGYDLDCGPVWDIIGPKDAKGLFSAKQDILLRTK 99
Db 11 QODLDNIVTWQPEVIQYDSGLCGYDEGCPVTFNIGSLDPKGLLSASKQDMIRKR 70
QY 100 MRECELLLOECAHQTTLKGRKVETITIIYDCEGLGLKHLWKPAVEAYGEFLCMFEENY 159
Db 71 IKVCELLHECELQTKLGRKIEMALMVDFMEGLSKHLWKPAVEYVQQFFSILEANYPE 130
QY 160 TLKRLFFVVKAPKLPFVAYNLIKPFLSEDRKKIMVIGANYKEVLLKHHISPDQVPVEYGGT 219
Db 131 TLKNLIVIRAPKLPFVAFNLVKSFMSSEETRRKIVILGDNWKQBELTKFISPDQLPVEFGT 190
QY 220 MTDPDGNPKCKSKINYGGDI PRKYVVRDQVKKQYEHVSQISRGSSHQVEYBILFPGCVLR 279
Db 191 MTDPDGNPKCLTKKINYGGEVPKSYVLCQVRLQYEHTRSVGRGSSLOVENEILLFPGCVLR 250
QY 280 WQFMSDGDADVGFGLFKTKMGERQAGTEVLNQRVNSHLVPEDGTLTCSDDPGIYV 337
Db 251 WQFMSDGGDVGFGVFLTKMGERQAGTEVLNQRVNSHLVPEDGTLTCLQAGVYV 308


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; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28170
; TYPE: PRN
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(478)
; OTHER INFORMATION: Ceres Seq. ID no. 2705654
US-11-096-568A-28170

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Query Match      11.0%; Score 221.5; DB 11; Length 478;
Best Local Similarity 26.8%; Pred. No. 6.1e-13;
Matches 70; Conservative 44; Mismatches 116; Indels 31; Gaps 6;

QY 31 SGMWSSEK-----RTLTS LAWQPEVIQQYLSGMCYDLDGCPVWYDIIGPKDA 83
DB 16 TNQMSDMLRWKKEFGADTVMEDEFKEDVLKYYPQGHGVKGRPVYIERLGQVDS 75

QY 84 KGLLFSASKQDLLRTKMRCE-----LLQEC AHQTTKLGKRVETITIIYDC EGLGKLHLM 139
DB 76 TKLMQVTTMDRYVNVHMEFERTFNVPKPAACIAAK--HIDQSTTILDVQGVGLKNFN 132

QY 140 KPAVEAYGEFLCMFEENYPETLKR LFPVVKAPKLPFVAYNLKPF LSEDT RKKIMVLGANY 199
DB 133 KAARDLITRLQKVDGNDYPETLNR MFIINAGSGFRMLMNTVKSFLDPKTTAKIHLGNKY 192

QY 200 KEVLLKHISPDQVPVEYGGTWT-----DPDGNPKCKSKINYGDDIPRKYVYRD 247
DB 193 QSKLLEIIDASELPFLGSGCTCADNGGCMRSDKGPWNNPDIMKRVNNGDHICSK---RS 249

QY 248 QVKQYEHVSQISRGSSHOVE 268
DB 250 QADNAGENI--ISQGNNSAVE 268

```

```

RESULT 8
US-11-096-568A-28169
; Sequence 28169, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28169
; TYPE: PRN
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(517)
; OTHER INFORMATION: Ceres Seq. ID no. 2705653
US-11-096-568A-28169

```

```

Query Match      11.0%; Score 221.5; DB 11; Length 517;
Best Local Similarity 26.8%; Pred. No. 6.8e-13;
Matches 70; Conservative 44; Mismatches 116; Indels 31; Gaps 6;

QY 31 SGMWSSEK-----RTLTS LAWQPEVIQQYLSGMCYDLDGCPVWYDIIGPKDA 83
DB 55 TNQMSDMLRWKKEFGADTVMEDEFKEDVLKYYPQGHGVKGRPVYIERLGQVDS 114

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QY 84 KGLLFSASKQDLLRTKMRCE-----LLQEC AHQTTKLGKRVETITIIYDC EGLGKLHLM 139
DB 115 TKLMQVTTMDRYVNVHMEFERTFNVPKPAACIAAK--HIDQSTTILDVQGVGLKNFN 171

QY 140 KPAVEAYGEFLCMFEENYPETLKR LFPVVKAPKLPFVAYNLKPF LSEDT RKKIMVLGANY 199
DB 172 KAARDLITRLQKVDGNDYPETLNR MFIINAGSGFRMLMNTVKSFLDPKTTAKIHLGNKY 231

QY 200 KEVLLKHISPDQVPVEYGGTWT-----DPDGNPKCKSKINYGDDIPRKYVYRD 247
DB 232 QSKLLEIIDASELPFLGSGCTCADNGGCMRSDKGPWNNPDIMKRVNNGDHICSK---RS 288

QY 248 QVKQYEHVSQISRGSSHOVE 268
DB 289 QADNAGENI--ISQGNNSAVE 307

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RESULT 9

```

US-11-096-568A-28168
; Sequence 28168, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28168
; LENGTH: 558
; TYPE: PRN
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(558)
; OTHER INFORMATION: Ceres Seq. ID no. 2705652
US-11-096-568A-28168

```

```

Query Match      11.0%; Score 221.5; DB 11; Length 558;
Best Local Similarity 26.8%; Pred. No. 7.6e-13;
Matches 70; Conservative 44; Mismatches 116; Indels 31; Gaps 6;

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QY 31 SGMWSSEK-----RTLTS LAWQPEVIQQYLSGMCYDLDGCPVWYDIIGPKDA 83
DB 96 TNQMSDMLRWKKEFGADTVMEDEFKEDVLKYYPQGHGVKGRPVYIERLGQVDS 155

QY 84 KGLLFSASKQDLLRTKMRCE-----LLQEC AHQTTKLGKRVETITIIYDC EGLGKLHLM 139
DB 156 TKLMQVTTMDRYVNVHMEFERTFNVPKPAACIAAK--HIDQSTTILDVQGVGLKNFN 212

QY 140 KPAVEAYGEFLCMFEENYPETLKR LFPVVKAPKLPFVAYNLKPF LSEDT RKKIMVLGANY 199
DB 213 KAARDLITRLQKVDGNDYPETLNR MFIINAGSGFRMLMNTVKSFLDPKTTAKIHLGNKY 272

QY 200 KEVLLKHISPDQVPVEYGGTWT-----DPDGNPKCKSKINYGDDIPRKYVYRD 247
DB 273 QSKLLEIIDASELPFLGSGCTCADNGGCMRSDKGPWNNPDIMKRVNNGDHICSK---RS 329

QY 248 QVKQYEHVSQISRGSSHOVE 268
DB 330 QADNAGENI--ISQGNNSAVE 348

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RESULT 10

```

US-11-096-568A-32080
; Sequence 32080, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2

```

```
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32080
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(409)
; OTHER INFORMATION: Ceres Seq. ID no. 13592122
US-11-096-568A-32080

Query Match          10.7%; Score 216; DB 11; Length 409;
Best Local Similarity 22.2%; Pred. No. 1.6e-12;
Matches 94; Conservative 58; Mismatches 139; Indels 132; Gaps 17;

QY      5 VGDLSPRQKEAL--AKPEASTCSRSPRCGSMMS-----S 37
Db      41 VSELKPTQKSLQELKEKLSASSK---ASSMNGVSLGGDDKADVILLKFLRARDPKVA 97
QY      38 ESKRTLTTSLAWOPPEVIQY-----LSGG---MCGYDLGCPVWYDIIG---PKD 82
Db      98 DSLRMLEKCLEWREEFKAELTEEDLGFKDLEGKVAYMRGYDKEGHPVCYNAYGVFKEKE 157
QY      83 AKGLIFSASKQ--DLLRTKRECELLLOECAGHQTTLGRK-----VETITIIYDCEG 132
Db      158 MYERVFGEDEKLNKFLRWV-----QVLERGVKMLHPKPGGVNSIIQVTDLKD 205
QY      133 LGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLFVKAPKLPFVAYNLIKPFSLSDTRKK- 191
Db      206 MPKREL-----RVASNQILSLFDQNYPELVATKIFINVPWFVSIIYMSFPLTQRTSKFP 261
QY      192 IMVLGANYKEVLLKHLSPDQVPVEYGGTMTDPP---GNPKCKSKINYGDIIPRKYVVRDQ 248
Db      262 VMSKEGNAEATLYKFIREDIPVQYGLSRPTDSQNGPPKPASEFSIKG-----310
QY      249 VKQYEHVSQISRSSSHQVEYIILFPGCVLRWQPMSDGADVGFIFLTKMGERQORAGEM 308
Db      311 -----GEKVNIIQIEGGGATITWDIVVGGMDLEYS-----341
QY      309 TEVLNPNQRYNSHLVPED-----GTLTCSDPGIYVLRFDNTYSFIHAKKV---N 353
Db      342 AEFVFNABEESYAIIVKPKKMKATDEAVCNSTFTVEAGKLILSDVNTLS--RKKKVAAYR 399
QY      354 FTV 356
Db      400 YTV 402

RESULT 11
US-11-096-568A-32079
; Sequence 32079, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32079
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(433)
; OTHER INFORMATION: Ceres Seq. ID no. 13592121
US-11-096-568A-32079

Query Match          10.7%; Score 216; DB 11; Length 433;
Best Local Similarity 22.2%; Pred. No. 1.6e-12;
Matches 94; Conservative 58; Mismatches 139; Indels 132; Gaps 17;

QY      5 VGDLSPRQKEAL--AKPEASTCSRSPRCGSMMS-----S 37
Db      41 VSELKPTQKSLQELKEKLSASSK---ASSMNGVSLGGDDKADVILLKFLRARDPKVA 97
QY      38 ESKRTLTTSLAWOPPEVIQY-----LSGG---MCGYDLGCPVWYDIIG---PKD 82
Db      98 DSLRMLEKCLEWREEFKAELTEEDLGFKDLEGKVAYMRGYDKEGHPVCYNAYGVFKEKE 157
QY      83 AKGLIFSASKQ--DLLRTKRECELLLOECAGHQTTLGRK-----VETITIIYDCEG 132
Db      158 MYERVFGEDEKLNKFLRWV-----QVLERGVKMLHPKPGGVNSIIQVTDLKD 205
QY      133 LGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLFVKAPKLPFVAYNLIKPFSLSDTRKK- 191
Db      206 MPKREL-----RVASNQILSLFDQNYPELVATKIFINVPWFVSIIYMSFPLTQRTSKFP 261
QY      192 IMVLGANYKEVLLKHLSPDQVPVEYGGTMTDPP---GNPKCKSKINYGDIIPRKYVVRDQ 248
Db      262 VMSKEGNAEATLYKFIREDIPVQYGLSRPTDSQNGPPKPASEFSIKG-----310
QY      249 VKQYEHVSQISRSSSHQVEYIILFPGCVLRWQPMSDGADVGFIFLTKMGERQORAGEM 308
Db      311 -----GEKVNIIQIEGGGATITWDIVVGGMDLEYS-----341
QY      309 TEVLNPNQRYNSHLVPED-----GTLTCSDPGIYVLRFDNTYSFIHAKKV---N 353
Db      342 AEFVFNABEESYAIIVKPKKMKATDEAVCNSTFTVEAGKLILSDVNTLS--RKKKVAAYR 399
QY      354 FTV 356
Db      400 YTV 402

RESULT 12
US-11-096-568A-27441
; Sequence 27441, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27441
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: Ceres Seq. ID no. 1815699
US-11-096-568A-27441

Query Match          10.6%; Score 214; DB 11; Length 511;
Best Local Similarity 28.7%; Pred. No. 3.5e-12;
Matches 58; Conservative 35; Mismatches 95; Indels 14; Gaps 3;

QY      34 MWSSE-----SKRTLTTSLAWQPEVIQOYLSGGMCGYDLGCPVWYDIIGPKDAKGL 86
Db      57 MWSDMIQWRKDFGADTTIEDFDEIDVEMKHYQGVHGVDEKRPVIERLGQIDANKL 116
QY      87 LFSASKQDLRLTKMRECE---LILQECAGHQTTLGRKRETTITIIYDCEGLGLKHLWKPA 142
Db      117 LQVTTMDRYKYHYKREKFEKFKVPSCSVAANK---HIDOSTILDVQGVGLKNFSKA 173
QY      143 VEAYGEFLCMFEENYPETLKRFLFVKAPKLPFVAYNLIKPFSLSDTRKKIMVLGANYKEV 202
Db      174 RELQLRCKIDNENYPETLNRMFIIINAGSGFRLWSTVKSPLDPKTTAKIHVLGNKYHSK 233
```

```
Best Local Similarity 22.2%; Pred. No. 1.8e-12;
Matches 94; Conservative 58; Mismatches 139; Indels 132; Gaps 17;

QY      5 VGDLSPRQKEAL--AKPEASTCSRSPRCGSMMS-----S 37
Db      65 VSELKPTQKSLQELKEKLSASSK---ASSMNGVSLGGDDKADVILLKFLRARDPKVA 121
QY      38 ESKRTLTTSLAWQPEVIQY-----LSGG---MCGYDLGCPVWYDIIG---PKD 82
Db      122 DSLRMLEKCLEWREEFKAELTEEDLGFKDLEGKVAYMRGYDKEGHPVCYNAYGVFKEKE 181
QY      83 AKGLIFSASKQ--DLLRTKRECELLLOECAGHQTTLGRK-----VETITIIYDCEG 132
Db      182 MYERVFGEDEKLNKFLRWV-----QVLERGVKMLHPKPGGVNSIIQVTDLKD 229
QY      133 LGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLFVKAPKLPFVAYNLIKPFSLSDTRKK- 191
Db      230 MPKREL-----RVASNQILSLFDQNYPELVATKIFINVPWFVSIIYMSFPLTQRTSKFP 285
QY      192 IMVLGANYKEVLLKHLSPDQVPVEYGGTMTDPP---GNPKCKSKINYGDIIPRKYVVRDQ 248
Db      286 VMSKEGNAEATLYKFIREDIPVQYGLSRPTDSQNGPPKPASEFSIKG-----334
QY      249 VKQYEHVSQISRSSSHQVEYIILFPGCVLRWQPMSDGADVGFIFLTKMGERQORAGEM 308
Db      335 -----GEKVNIIQIEGGGATITWDIVVGGMDLEYS-----365
QY      309 TEVLNPNQRYNSHLVPED-----GTLTCSDPGIYVLRFDNTYSFIHAKKV---N 353
Db      366 AEFVFNABEESYAIIVKPKKMKATDEAVCNSTFTVEAGKLILSDVNTLS--RKKKVAAYR 423
QY      354 FTV 356
Db      424 YTV 426

RESULT 12
US-11-096-568A-27441
; Sequence 27441, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27441
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(511)
; OTHER INFORMATION: Ceres Seq. ID no. 1815699
US-11-096-568A-27441

Query Match          10.6%; Score 214; DB 11; Length 511;
Best Local Similarity 28.7%; Pred. No. 3.5e-12;
Matches 58; Conservative 35; Mismatches 95; Indels 14; Gaps 3;

QY      34 MWSSE-----SKRTLTTSLAWQPEVIQOYLSGGMCGYDLGCPVWYDIIGPKDAKGL 86
Db      57 MWSDMIQWRKDFGADTTIEDFDEIDVEMKHYQGVHGVDEKRPVIERLGQIDANKL 116
QY      87 LFSASKQDLRLTKMRECE---LILQECAGHQTTLGRKRETTITIIYDCEGLGLKHLWKPA 142
Db      117 LQVTTMDRYKYHYKREKFEKFKVPSCSVAANK---HIDOSTILDVQGVGLKNFSKA 173
QY      143 VEAYGEFLCMFEENYPETLKRFLFVKAPKLPFVAYNLIKPFSLSDTRKKIMVLGANYKEV 202
Db      174 RELQLRCKIDNENYPETLNRMFIIINAGSGFRLWSTVKSPLDPKTTAKIHVLGNKYHSK 233
```

Qy 203 LLKHISPDQVPVEYGGTMDPD 224
||:|::|:|:|
pb 234 LLEVIDASELPEFFGGACTCED 255

```

RESULT 13
US-11-096-568A-27440
; Sequence 27440, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA F
; TITLE OF INVENTION: Sequence-Determined DNA F
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27440
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(551)
; OTHER INFORMATION: Ceres Seq. ID no. 1815698
US-11-096-568A-27440

```

Query March	10.6%	Score 214;	DB 11;	Length 551;
Best Local Similarity	28.7%;	Pred. No. 3.9e-12;		
Matches 58;	Conservative 35;	Mismatches 95;	Indels 14;	Gaps 3;
Qy	34	MWSSE-----SKRTLTTSLAWQPPEVIOQYLSGSMCGYDLDCGPVMYDIIGPKDAKGL	86	
Db	97	MWSDWIQWRKDFGADTIIEDPFEIIDEVMKHYPQGYGVDDKEGRPVVIERLGGIDANKL	156	
Qy	87	LFSASKQDLLRTKWRCE-----LLLOECANHTTKLRKVETITIIYDCEGLGLKHLWKPA	142	
Db	157	LQVTTMDRYVKYHYHVKFEKTEKVPKPPSCSVAANK---HIDQSTWILDVQGVGLKNFSSKA	213	
Qy	143	VEAYGEFLCMEENYPETLKRFLVYVAKPLPPVAYNLIKPLFSBDTRKKIMVLGANYKEV	202	
Db	214	RELQRLCKINDENYPETLNRMFINDINAGSGPFLWSTVKSFLDPKTTAKIHVLGNKYHVK	273	
Qy	203	LLKHISPDQVPVEYGGTMTDDP	224	
Db	274	LLEVIDASELPFEFFGACTCED	295	

```

RESULT 14
US-11-096-568A-27439
; Sequence 27439, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA F
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592APUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27439
; LENGTH: 560
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(560)
; OTHER INFORMATION: Ceres Seq. ID no. 1815697
US-11-096-568A-27439

```

Query Match 10.6%; Score 214; DB 11; Length 560;
Best Local Similarity 28.7%; Pred. No. 4e-12;

[illegible]

```

RESULT 15
US-11-096-568A-9415
; Sequence 9415, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1552FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 9415
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(394)
; OTHER INFORMATION: Ceres Seq. ID no. 12460984
US-11-096-568A-9415

```

Query Match	10.6%	Score 213;	DB 11;	Length 394;
Best Local Similarity	24.9%	Pred. No. 3e-12;		
Matches	80;	Conservative 46;	Mismatches 147;	Indels 48; Gaps 10;
Qy	35	WSSE--SKRTLTTSIAWQPPEVILQQYLSGGWCGYDLDGCPWYDIIG---PKDAYKGLLFS	89	
Db	95	WRAEFADAVLDEDLGFGLLEGIVAY---MHGWRDRGHPVCYNAYGVFKDRMDYDRVFG	150	
Qy	90	ASKQDLLRTKWRCECLLQBCAHQTTKLGKRVKVTITIIYDCEGIGLGHKLWKPAVEAYGEF	149	
Db	151	DG--DRLSRFLRWVQIMERGVRAQLRPGGVNAIIQVTDLKDMPKREL----RAASNQI	204	
Qy	150	LCWFEENYPETLKLFLVVKAPKLPFVAYNALIKPLSEDTKIKINVL--GANYKEVLLKHIS	208	
Db	205	LSLFQDNPYEMVARKVFVNVPWFYFSVLFSMISPELTERTKSKFVIAREGNVAETLFKFIR	264	
Qy	209	PQQVPVBYGGTMTDPD---GNPKCKSKINYGDDIPRKYVYRDQVKQVQVHSGVQISRGSSH	265	
Db	265	PELVVPVQIGLGRASELENGPPKPASEFTIKG-----GKVV	300	
Qy	266	QVEYEILFPGCVLRQWMSGDADVGFGI--FLTKTKGQRQRAGETVFLPNQRYNSHLVPE	324	
Db	301	FLEIDGIEAGATITDWLVVGWELEYGAEYVPASEGGYTLCLVERTKKVPAAADE----PV	356	
Qy	325	DGTLTCDSPDGIYVLPFDNTYS	345	
Db	357	HNAFTAKEPGKWLISIDNSGS	377	

Search completed: May 2, 2006, 18:53:58
Job time : 28 secs

PEASTCRSRRRPCSGSMWSSSKRTLTTSLA

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 2, 2006, 18:34:32 ; Search time 40 Seconds
(without alignments)
909.248 Million cell updates/sec

Title: US-10-696-699A-2
Perfect score: 2018
Sequence: 1 MGRVGDLSPRQKEALAKPE.....LLPDKASEEKKQLGAGTPK 378

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1827.5	90.6	403	2 JC7708	tocopherol associa
2	661.5	32.8	343	2 A53057	retinal-binding pr
3	408	20.2	383	2 T23057	hypothetical prote
4	388.5	19.3	470	2 S28303	hypothetical prote
5	388.5	19.3	743	2 B88551	protein T23G5.2 [i
6	334	16.6	1254	2 T24897	hypothetical prote
7	229.5	11.4	490	2 A96745	probable cytosolic
8	229	11.3	457	2 C86329	hypothetical prote
9	228	11.3	286	2 T38768	probable sec14 cyt
10	221.5	11.0	558	2 C84561	hypothetical prote
11	218	10.8	582	2 F84539	hypothetical prote
12	217.5	10.8	371	2 E84602	hypothetical prote
13	216	10.7	409	2 T46063	hypothetical prote
14	214	10.6	560	2 T05278	hypothetical prote
15	210	10.4	301	2 S57923	SEC14 protein - ye
16	210	10.4	310	2 S37916	SEC14 protein homo
17	207	10.3	558	2 G85430	hypothetical prote
18	206.5	10.2	531	2 C84602	hypothetical prote
19	204.5	10.1	396	2 T33386	hypothetical prote
20	203	10.1	723	2 H85092	hypothetical prote
21	199.5	9.9	550	2 T08566	hypothetical prote
22	197	9.8	304	2 A30106	SEC14 protein - ye
23	188	9.3	341	2 G89500	protein T27A10.7 [
24	183.5	9.1	640	2 B96784	hypothetical prote
25	181	9.0	278	1 A47404	alpha-tocopherol t
26	181	9.0	278	2 S54352	alpha-tocopherol t
27	179	8.9	377	2 T21170	hypothetical prote
28	179	8.9	453	2 T21528	hypothetical prote
29	176.5	8.7	497	2 S43745	phosphatidylinosit

SEC14 protein - ye
hypothetical prote
hypothetical prote
probable cytosolic
hypothetical prote
phosphatidylinosit
hypothetical prote
F12K8.13 protein -
hypothetical prote
hypothetical prote
polyphosphoinosit
SEC14 protein homo
hypothetical prote
protein F14J16.8 [i
hypothetical prote
hypothetical prote

ALIGNMENTS

RESULT 1

JC7708
tocopherol associated protein - human
N;Alternate names: alpha-tocopherol associated protein
C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C;Accession: JC7708
R;Yamauchi, J.; Iwamoto, T.; Kida, S.; Masushige, S.; Yamada, K.; Esashi, T.
Biochem. Biophys. Res. Commun. 285, 295-299, 2001
A;Title: Tocopherol-associated protein is a ligand-dependent transcriptional activator.
A;Reference number: JC7708; MUID:21338208; PMID:11444841
A;Contents: Liver
A;Accession: JC7708
A;Molecule type: mRNA
A;Residues: 1-403 <YAM>
A;Cross-references: UNIPROT:O76054; UNIPARC:UPI000017CBA2; GB:AL096881
C;Comment: This protein has the following properties: (i) alpha-tocopherol specific bin
driptional activation involved in gene regulation in vivo in mammalian cells.
C;Genetics:
A;Gene: tap

Query Match	90.68;	Score	1827.5;	DB 2;	Length	403;			
Best Local Similarity	87.1%;	Pred. No.	2.4e-147;						
Matches	351;	Conservative	9;	Mismatches	18;	Indels	25;	Gaps	2;
Qy	1	MSGRVGDLSPRQKEALAK-----PEASTCRSRRPCSGSMWSSS-----	39						
Db	1	MSGRVGDLSPRQKEALAKFRENVDVLPALPNPDHFLRLRLARSFDLQKSEAMLRKHV	60						
Qy	40	-----KRTLTTSLAWQPEVITQOYLSGCMCGYDLDGCPVWYDIIGPKDAKGLLPFSASKQDL	95						
Db	61	EFRKQKDIDNIIISQPPVITQOYLSGCMCGYDLDGCPVWYDIIGPLDAKGLLPFSASKQDL	120						
Qy	96	LRTKMRCELLQECACHQTTKLRKVKETITIIYDCEGLGLKHLWKPAVEAYGEFLCMFEE	155						
Db	121	LRTKMRCELLQECACHQTTKLRKVKETITIIYDCEGLGLKHLWKPAVEAYGEFLCMFEE	180						
Qy	156	NYPETLKRFLFVVKAPKLPFPVAYNLIKPFLSEDTTRKKIMVLGANYKVELLKHISPDQVPVE	215						
Db	181	NYPETLKRFLFVVKAPKLPFPVAYNLIKPFLSEDTTRKKIMVLGANYKVELLKHISPDQVPVE	240						
Qy	216	YGGTMTDPGNPKCKSKINTYGGDIPRKYYVRDVKQYEHVSQISRGSSHQVEYELLPPG	275						
Db	241	YGGTMTDPGNPKCKSKINTYGGDIPRKYYVRDVKQYEHVSQISRGSSHQVEYELLPPG	300						
Qy	276	CVLRWQFMSGADVGFGLFKTKMGERQAGEMTEVLPNQRYNSHLVPEDGTLTCSDPGI	335						
Db	301	CVLRWQFMSGADVGFGLFKTKMGERQAGEMTEVLPNQRYNSHLVPEDGTLTCSDPGI	360						
Qy	336	YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK	378						
Db	361	YVLRFDNTYSFIHAKKNFTVEVLLPDKASEEKKQLGAGTPK	403						

```
RESULT 2
A:3057
retinal-binding protein - Japanese flying squid
C:Species: Todarodes pacificus (Japanese flying squid)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A53057
R:Ozaki, K.; Terakita, A.; Ozaki, M.; Hara, R.; Hara, T.; Hara-Nishimura, I.; Mori, H.;
J. Biol. Chem. 269, 3838-3845, 1994
A:Title: Molecular characterization and functional expression of squid retinal-binding p
A:Reference number: A53057; MUID:94148895; PMID:8106428
A:Accession: A53057
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-343 <OZA>
A:Cross-references: UNIPROT:P49193; UNIPARC:UPI000016C018; GB:S68871; NID:G545382; PID:9
A:Experimental source: eye
A>Note: sequence extracted from NCBI backbone (NCBIN:143812, NCBI:P:143813)

Query Match 32.8%; Score 661.5; DB 2; Length 343;
Best Local Similarity 37.2%; Pred. No. 2.2e-48;
Matches 122; Conservative 82; Mismatches 115; Indels 9; Gaps 2;

QY 49 WQPPEVIQOYLSSGCMGYDLDCGPVWYDIIGPKDAKGLLFSASKODLLRTKMRCELLQ 108
DB 16 YTPPDVIOKMTGGDVGHDKDGSVLRIPWGYLDMKIMYSCKSDLEKSKLLQCEKHL 75
QY 109 ECAHOTTKLGRKVTITIIYDCGELGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLV 168
DB 76 DLEAQSEKVGKCTGTVTVFDMENVGSKHMKPGLDMDYLVQVLEDNYPENMKRLFVN 135
QY 169 APKLFPVAYNLKPKFLESDTRKKIMVLGANYKEVLLKHISPDQVPVEYGGTMTDPGNPK 228
DB 136 APTLPVLKLVKPLLESDMKNKIFVLGGDYKDTLLLEYIDAEELPAYLGSTKS--EGDEK 193
QY 229 CKSKINYGGDIPRKYYVRDQVK--QQYEHVQISRGSSHQVEYELPFGCVLRFVVK 288
DB 194 CSELICHGGEVPEKPYLENTDFMETITVSGGDKIYVEYEIENENTYIKWEYKTEHD 253
QY 289 VGFGLTKTKMERQAGTEVLPNORYNSHLVPEDGTLTCSDPGIVVLRFDNTYSFTH 348
DB 254 IGFGLF-----RKNGDWEEVVPPIERTDCSIMTLDGSHKCKDPETALCFDNSFSMT 306
QY 349 AKKYNFTVEVLLPDKASEKMKQLGAGT 376
DB 307 SKNVRVTAEVMDPEVDSEINKMKWDST 334

RESULT 3
T23057
hypotheical protein H06001.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23057
R:Barlow, K.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19665
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:Cross-references: UNIPROT:O17907; UNIPARC:UPI0000078A7E; EMBL:Z92970; PIDN:CAB07482.1;
A:Experimental source: clone H06001
C:Genetics:
A:Gene: CESP:H06001.3
A:Map position: 1
A:Introns: 21/2; 75/3; 137/3; 190/2; 219/3; 302/2; 358/1

Query Match 20.2%; Score 408; DB 2; Length 383;
Best Local Similarity 29.6%; Pred. No. 8.9e-27;
Matches 93; Conservative 71; Mismatches 142; Indels 8; Gaps 7;

QY 49 WQPPEVIQOYLSSGCMGYDLDCGPVWYDIIGPKDAKGLLFSASKODLLRTKMRCELLQ 108
DB 71 WTPPECLEKYGCGYGLLG--DTEGRFILMSLLGNVDVEGLRSVASLDYIKFSLAAIEKGMK 129
QY 109 ECAHOTTKLGRKVTITIIYDCGELGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLV 167
DB 130 LCEEKAKESGRPFQMTLVFDLENITSAHSCFKQPASSFTLLVSLFQDHYPLFLKILLI 189
QY 168 KAPKLPVAYNLKPKFLESD--TRKKIMVLGANYKEVLLKHISPDQVPVEYGGTMTDPGN 226
DB 190 RAPEMARITAYASITAILQDPIITRLVEMPSESDMKWSLAQIVNLDAWPMVWGGLNVE--NGD 248
QY 227 PKCKSKINYGGDIPRKYYVRDQVK--QQYEHVQISRGSSHQVEYELPFGCVLRFVVK 284
DB 249 PKCPSRIKYGGADESIFYDPKKAMADYDQLTTVYAGDKHLIQIKVXRPSPRI--SWTYMT 307
QY 285 DGADVGFGLTKMERQAGTEVLPNORYNSHLVPEDGTLTCSDPGIVVLRFDNTY 344
DB 308 DEDDIDGFEIHY-DKGTGSCDKLTEMETVYPIRLECTNVPITGHLDVTDVGNVLEFDNYY 366
QY 345 SFIHAKKNFTVEV 358
DB 367 SWFSAKQLRYNIEI 380

RESULT 4
S28303
hypotheical protein T2305.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28303
R:Berks, M.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28296
A:Accession: S28303
A:Molecule type: DNA
A:Residues: 1-470 <BER>
A:Cross-references: UNIPROT:Q03606; UNIPARC:UPI000017BBE0; EMBL:Z19158
C:Genetics:
A:Introns: 209/3; 322/3; 389/3; 439/2
F:32-240/Domain: cellular retinaldehyde-binding protein homology <CRB>

Query Match 19.3%; Score 388.5; DB 2; Length 470;
Best Local Similarity 28.2%; Pred. No. 5.3e-25;
Matches 106; Conservative 59; Mismatches 136; Indels 75; Gaps 10;

QY 49 WQPPEVIQOYLSSGCMGYDLDCGPVWYDIIGPKDAKGLLFSASKODLLRTKMRCELLQ 108
DB 68 WTRPTVIKQYFPGCWHNSDKAGRPWYIIRFGQDITKGLRSCGVENLVKLTLSICEDGLQ 127
QY 109 ECAHOTTKLGRKVTITIIYDCGELGLKHLWKPAVEAYGEFLCMFEENYPETLKRFLVVK 168
DB 128 RAAEATRKLGTPISSWSLVVDLDGLSMRHLWRPGVQCLLKIIIEVANYPETMGQVLVVR 187
QY 169 APKLFPVAYNLKPKFLESDTRKKIMV---LGANYKEVLLKHISPDQVPVEYGGTMTDPG 225
DB 188 APRVFPVLTLISPFIDEXTRKKFMVSGSGDGLKEELRKHTEEFKIPDFLGGSC----- 242
QY 226 NPKCKSKINYGGDIPRKYYVRDQVKQYEHVQISRGSSHQVEYELPFP----- 274
DB 243 ---LTTNCGLGHVPKSNYL--PVEQEGASSEDPLHSTYTSTATWGRYPVEVPIET 297
QY 275 -GCVLRLWFMSDAGDVGFIPLTKWGE-----RQAGEMTEVL-----PNOR 316
DB 298 AGCVLTWDFDLVKNDCEFSLVFSTEKIEQPAVRDGAQSPPTTLNPNVEMVMSAAIGGASHOH 357
QY 317 YNSHLVPE-----DGLTLCSDPGIYVLR-----DNTY 344
DB 358 PDLQCAPELKIQTGPQLRLEEKAVVQEGDSMQGSHYCSRAGTYIMQWRVPETAAGHSSTF 417
QY 345 SF-IHAKKNFTVEV 359
DB 418 DFGSHKRLIYVYIEL 433
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A;Map position: 5
A;Introns: 63/1; 158/2; 200/3; 286/2; 404/3; 437/1; 539/3; 616/1; 688/3; 732/3; 778/3; 816/1; 888/2; 958/3; 1028/2; 1108/3; 1188/2; 1268/3; 1348/2; 1428/3; 1508/2; 1588/3; 1668/2; 1748/3; 1828/2; 1908/3; 1988/2; 2068/3; 2148/2; 2228/3; 2308/2; 2388/3; 2468/2; 2548/3; 2628/2; 2708/3; 2788/2; 2868/3; 2948/2; 3028/3; 3108/2; 3188/3; 3268/2; 3348/3; 3428/2; 3508/3; 3588/2; 3668/3; 3748/2; 3828/3; 3908/2; 3988/3; 4068/2; 4148/3; 4228/2; 4308/3; 4388/2; 4468/3; 4548/2; 4628/3; 4708/2; 4788/3; 4868/2; 4948/3; 5028/2; 5108/3; 5188/2; 5268/3; 5348/2; 5428/3; 5508/2; 5588/3; 5668/2; 5748/3; 5828/2; 5908/3; 5988/2; 6068/3; 6148/2; 6228/3; 6308/2; 6388/3; 6468/2; 6548/3; 6628/2; 6708/3; 6788/2; 6868/3; 6948/2; 7028/3; 7108/2; 7188/3; 7268/2; 7348/3; 7428/2; 7508/3; 7588/2; 7668/3; 7748/2; 7828/3; 7908/2; 7988/3; 8068/2; 8148/3; 8228/2; 8308/3; 8388/2; 8468/3; 8548/2; 8628/3; 8708/2; 8788/3; 8868/2; 8948/3; 9028/2; 9108/3; 9188/2; 9268/3; 9348/2; 9428/3; 9508/2; 9588/3; 9668/2; 9748/3; 9828/2; 9908/3; 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